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A Computational Study of the Emergent Properties of Self-Producing Systems

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Abstract

The theory of autopoiesis (auto - self, poiesis - producing) suggests that a living system distinguishes itself from non-living matter by its ability to generate and maintain itself. With the increase in systems thinking and complexity science at the turn of the twenty-first century, this idea has been steadily gaining traction in fields as diverse as biology, the social sciences, law and architecture. The theory has been adopted most widely in the field of synthetic biology and chemistry where it provides a conceptual framework within which to understand the organisational logic of minimal living cells (protocells). The potential of autopoiesis to inform protocell research is dependent on a greater understanding of the organisational pathways that may lead to the formation of the most basic autopoietic systems. A computational study into the formation and persistence of proto-autopoietic organisations from simple, unstructured beginnings is reported here.

Computer simulations show that unstructured populations of interacting finite state automata self-organise under different environmental conditions to robust, self-producing structures called niches. The criteria for an autopoietic system remains a contested issue in the field and, as such, these niches could not be deemed to be fully autopoietic although they did routinely demonstrate the critical processes of self-production and adaptation. Competition at the individual, networked and niche level operated on such processes and was responsible for the continuous transformation of the population's structure in response to changes in the environment. Such structural coupling ensured the maintenance of the organisational identity of the proto-autopoietic system - the hallmark of autopoiesis - which was enabled by the emergence of hierarchical, strongly connected and dynamically stable networks that proved resilient to major environmental perturbations.

This work has tested the hypothesis that autopoietic systems can emerge from simple, unstructured beginnings. The research findings uphold this hypothesis, and several important features and properties of proto-autopoietic systems have also been reported. This research has shown that proto-autopoietic organisations are generated and maintained through competitive production processes and protocell researchers may wish to consider this in the design of their experimental strategies.

DEDICATION AND ACKNOWLEDGEMENTS

I dedicate this work to the memory of my grandfather John Wiltshire from whom I inherited my ceaseless curiosity and inquisitiveness about the world. My grandfather was a World War II army veteran who was one of the fortunate to be evacuated from the beaches of Dunkirk and less fortunate to be re-deployed to North Africa where he was captured and transferred as a prisoner of war to the Auschwitz camp in Poland. At the end of the war he undertook a so-called 'death march' to freedom where he experienced yet more unforgettable horrors of what humans can do to each other. Throughout such difficult trials his passion for knowledge and understanding continued and he would often raise his eyes to the night sky and wonder where else life could exist in the universe. For him there was no question 'if'. To him I dedicate this work which, in its own small way, is a modest contribution to the conversation on the origin of life.

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AUTHOR'S DECLARATION

I declare that the work in this dissertation was carried out in accordance with the requirements of the University's Regulations and Code of Practice for Research Degree Programmes and that it has not been submitted for any other academic award. Except where indicated by specific reference in the text, the work is the candidate's own work. Work done in collaboration with, or with the assistance of, others, is indicated as such. Any views expressed in the dissertation are those of the author.

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CHAPTER 1

INTRODUCTION

Natural selection may explain the survival of the fittest, but it cannot explain the arrival of the fittest. - Hugo De Vries in *Species and Varieties: Their Origin by Mutation (1904)*

1.1 Context

The theory of cellular life proposes that biological cells are the essential building blocks for living systems, with the single cell subjected to Darwinian evolution being the primary unit for life [1]. This raises the circular question of how the first living cells emerged in the absence of established biological evolution. The Russian chemist - Alexander Oparin - developed the concept of 'molecular evolution as the chemical progenitor of biological evolution' [2] and this has come to be the basis for modern research into the origin of life. Specifically, Oparin proposed [3] that initially simple abiotic molecules spontaneously formed more complex molecular chemistries. This may lead to the emergence of the primitive processes of replication, metabolism and compartmentalisation which would be a critical step on the pathway to the emergence of the first living cells. Such a primitive system would need to operate in a manner that maintained and increased its viability

in the presence of selective pressures. In this way it is envisaged that such a system would evolve as it endured and adapted under various environments. This would be a form of autonomous chemical system and that has been conceptualised as a protocell [4]. The need for a systems perspective on protocell formation has led to the emergence of the discipline of systems chemistry which focuses on the development of molecular systems that demonstrate emergent properties that are only possible through the collective behaviour of the interacting molecules that constitute the chemical system of interest.

"One of the grand challenges of Systems Chemistry, namely producing synthetic life, might be fulfilled through the design of a collection of molecules, a 'network', that is simple enough to self-organize, yet sufficiently complex to accommodate the essential properties of a living organism: compartmentalisation, replication and metabolism, all maintained out-of-equilibrium." [5]

As a discipline still in its infancy, systems chemists do not yet have a definitive body of knowledge of which design strategies (e.g. chemical affinities, reaction network structures, feedback loops, and so on) would be likely to achieve such outcomes. Nevertheless, attempts have been made to define a system architecture deemed to be most closely aligned to this aim and one of the more prominent and convincing models is based on the theory of autopoiesis [6].

The theory of autopoiesis [7] - from the Greek *auto-* meaning 'self' and *poiesis* meaning 'production' - was developed by the Chilean biologists Humberto Maturana and Francisco Varela who proposed that living systems are distinguished from non-living systems by the ability to continually reproduce and maintain themselves. In this concept an autopoietic system consists of entities that interact with each other to produce new entities which are identical to those that participated in the process. In other words, an autopoietic system produces the components of which it is composed and this results in a system that can persist over time as it produces new entities as old entities decay. A key characteristic of an autopoietic system is that it creates an interface between its interior - containing the entities of the production process - and its environment. The characteristic model of an autopoietic system is a biological cell whereby the process of production creates a membrane that encapsulates the internal reaction networks that produce the entities that constitute the membrane. This circularity gives rise to a self-contained system that is operationally closed. The relationships between the entities of such a system is called the *organisation* of the autopoietic system and the specific arrangement and configuration of those entities at any moment in time is its *structure*.

A conceptual example of an autopoietic organisation is a chemistry consisting of three components [6] - a substrate, a product and a waste product - that collectively are sufficient

to form and maintain a boundary that encapsulates the reactions that are required to produce the boundary. A schematic of such a minimal autopoietic cell is shown in Figure 1.1.

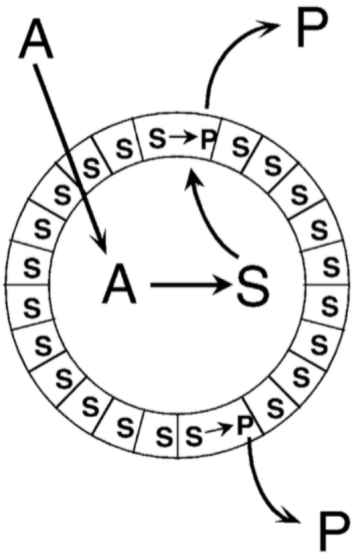

Figure 1.1: Luisi's schematic of a minimal autopoietic cell where a substrate entity (A) produces the product (S) which links to other S entities to form a boundary which encapsulates the $A \rightarrow S$ reaction. Over time S decays to the waste product (P) leaving a hole in the boundary which is repaired by another S molecule generated from the internal reaction. Taken from [8].

This artificial chemistry was first simulated by Francisco Varela in 1974 [9] and has since been examined in detail [10],[11] with more recent simulations emphasising the physical accuracy of the reactions and the transport of artificial chemistries. The boundary of an autopoietic system does more than act as a compartment. It also acts as a mediating interface with the environment that through a sensorium [2] allows an exchange of matter and information between the interior and the exterior. This exchange can trigger changes to the structure of the autopoietic cell which, in turn, can lead to a change in the state of the system. Some of these changes may be transitory, with no long term effect on the system, whilst others may be persistent and that permanently change the structure (but not the organisation) of the system. This plasticity [8] is an important characteristic of an autopoietic system as it allows the system to adapt to its environment. Of course, a change in behaviour of an open system such as an autopoietic cell will lead to changes in the environment through altered emissions (as waste product or information) from the cell itself. Such structural coupling between cell and environment is a reflexive cycle i.e. the autopoietic system forms and is formed by its environment. This process of adaptation is

called cognition and has been studied extensively [12],[13],[14],[2],[15],[16]. It is the main mechanism by which an autopoietic system is claimed to evolve [7]. The combination of cognition with the process of autopoiesis (self-production) constitutes and maintains the organisation of the system.

The main strengths of the theory of autopoiesis are that: (a) the concept is sufficiently abstract and agnostic to the chemical systems or molecules by which an autopoietic system can be realised. Together these provide the desirable quality of minimality which, when seeking to model the formation of a basic living system, is to be favoured; and (b) it is a scalable concept that has explanatory power through all of the major evolutionary transitions [17] from the most basic living cell to human cognition to social systems. It has generated interest outside of its field of origin (biology) and been applied to social systems [18], art [19], knowledge in institutions [20], computation theory [21], information systems [22], law [23] and architecture [24].

However, the adoption of autopoietic theory within biology has had a somewhat slow uptake primarily because it arrived at a time in the early 1970's when a reductionist paradigm was prevalent in the field with research efforts focused on the extrapolation of the genome to explain biological behaviour. Nevertheless towards the end of the twentieth century and with the increasing attention being given to system sciences - particularly systems biology and complexity science - autopoiesis began to be recognised as a concept that was somewhat ahead of its time [6]. Within the specialised field of neurobiology and cognitive sciences autopoiesis is now widely accepted as a central tenet of embodied cognition theory [25]. Within the relatively new field of synthetic biology autopoiesis has been adopted as a popular model of the system logic of a minimal living cell (the so-called protocell) [26]. By comparison, within the field of evolutionary biology autopoiesis has still not been recognised as part of the theoretical firmament alongside DNA and Darwinian evolution (the so-called modern synthesis) nor does it form part of the ongoing extended evolutionary synthesis movement. This has been investigated [27] with the conclusion that the lack of clarity and the under-developed nature of the relationship between autopoiesis and Darwinian evolution is the main issue. Attempts have been made to relate these two fields [7], [28], [29], [30]; however, a clear understanding of the relationship remains elusive. Subsequently autopoiesis remains an outlier in evolutionary biology research. As a case in point a recent review of the extended evolutionary synthesis [31] makes no mention or reference to autopoiesis or any related works even though the authors state the fundamental importance of 'constructive processes' to developing the field of biology. As will be discussed in Chapter 2 autopoiesis is intrinsically and fundamentally a constructive process and so its continued omission from the conversation on evolutionary

biology warrants attention.

My view, which is introduced here but which unfolds throughout this thesis, is that the state-of-the-art in the field of autopoiesis research does not directly address nor sufficiently explain *how* autopoietic systems may form from simple, unstructured beginnings. Or, in other words, given the innate power of autopoiesis theory to explain constructive processes it does not adequately explain the origin of itself. Maturana & Varela [32] describe the coming together of three concurrent processes (metabolism, compartmentation and adaptation) but they omitted to address where and how these processes could have emerged. The artificial chemistries used to demonstrate the formation of a minimal autopoietic cell [9] - and to prove the concept of autopoiesis - rely entirely on the presence of an ideal chemistry. Yet from where could such a chemistry have emerged? We could assume, no matter how improbable, that such a chemistry could occur spontaneously given a sufficiently diverse population of chemicals able to interact over very large timescales [1] but this dodges the question and effectively 'kicks the can down the road'. The hypothesis that needs to be tested is that autopoietic systems form from a pathway that originated from simple, undefined and unstructured beginnings. Such a system may become increasingly structured over time and such an organised chemical system may act as a resilient platform from which various candidate autopoietic organisations could be trialled and tested. Such platforms would themselves need to demonstrate a degree of self-maintenance and renewal simply to sustain themselves in an external environment. As such, these platforms would need to exhibit autopoietic-like behaviour without actually being fully autopoietic. I call these proto-autopoietic systems. With this simple distinction in mind we can now ask questions such as:

- What construction occurs *prior* to the formation of a fully autopoietic system?
- What are the organisational pathways from very simple organisations to those that begin to exhibit proto-autopoietic behaviour?
- What are the properties of proto-autopoietic systems?
- How do such properties emerge from simple, undefined beginnings?
- Do such proto-autopoietic systems endure?
- Is it possible that fully autopoietic systems could form from these proto-autopoietic states?

[1] Stuart Kauffman's work on the emergence of autocatalytic sets attempts to answer such questions and this is discussed in Chapter 2.

- At what point does a proto-autopoietic system become a fully-fledged autopoietic system?

Such proto-autopoietic states need to be understood if we are to explain how autopoietic systems may have formed on the early earth and before the arrival of the first living cell.

The purpose of this project is to investigate the possible pathways to autopoiesis. The contribution that this research may make, is to suggest a theory for the origin of autopoietic forms of organisation.

1.2 Research Aims

The research questions that this project sought to answer and the related aims of this project were:

Research Question	Research Aim
Q1. Can autopoietic systems form from simple, unstructured beginnings?	State the criteria and method for evaluating whether a system has achieved autopoiesis. Maturana & Varela originally proposed such criteria [7] which was subsequently refined [6]. The criteria for a physical boundary remains a contested issue [33] and this will be discussed in Chapter 2
Q2. If they exist, what pathways emerge and what are their properties?	Develop a minimal computational model that supports an interacting population coupled to an environment. This will require a model that distinguishes an internal environment (i.e. the positions of the interacting entities in time and space) from an external environment (i.e. those global parameters that perturb the internal environment). It is important that the chosen model and methodology strike the right balance between being minimal enough to avoid any claim of over-engineering the results and yet able to demonstrate non-trivial and interesting behaviours. Design a strategy for identifying and measuring any emergent properties of an evolving population of interacting entities. Both quantitative and qualitative approaches should be considered

Q3. If they exist, why and how do these pathways form?	The model must have a temporal dimension from which a variety of time-series data can be generated e.g. changes in structure of a population over time, growth and decay of interaction networks, changes in the composition and/or diversity of the population. State their limitations and review the impact that this may have on supporting the formation of autopoietic systems. Review the results from simulations and define the properties of proto-autopoietic structures as a springboard from which fully autopoietic systems may emerge
Q4. What contribution does this make to the theory of autopoiesis?	Identify and state clearly the current limitations of the theory of autopoiesis and its application. State which limitations this work addresses e.g. provide more insight into the origin of autopoietic systems
Q5. What contribution does this make to the origin of life?	Review the state-of-the-art in the theoretical approaches to defining a living system and clearly outline the current limitations in the field especially where it relates to autopoiesis
Q6. Can autopoietic theory contribute more than it has to evolutionary theory?	The project should consider the perceived limitations of autopoietic theory in extending our understanding of evolutionary processes. Furthermore, consideration should be given to whether a greater understanding of the origin of autopoietic systems can provide new insights into evolutionary biology
Q7. How can a better understanding of the formation of autopoietic structures benefit experimental work on protocells?	Consider the impact that any findings may have on experimental work to chemically construct protocells

Table 1.1: Research questions and aims.

1.3 Rationale

This project examines how a simple, initial population of interacting entities may become more structured over time. The phenomena of self-organisation and emergence are the two concepts from the field of complexity science - which is the study of the phenomena arising from large numbers of interacting entities [34] - that capture the behaviour that will need to be reproduced. As such this project takes a complexity science approach to examining the formation of self-organising networks that may demonstrate autopoietic properties. A common method in complexity science is to reproduce the behaviour of a system of interest through simulating a computational model. Such an approach makes it possible for a large number of entities to interact concurrently under environmental conditions that vary in "real time". Such variations are not plausible using analytical methods such as the numerical simulation of a system of differential equations.

Two of the main tools in the complexity scientist's toolbox that are valuable for this project are information theory and network theory. The former provides a way to quantitatively measure the complexity of a process, a structure or a collection of entities whilst the latter provides a concise mathematical approach to quantifying the relationships between large numbers of entities. Both approaches are required to record and define the structures and processes that may emerge as a simple population self-organises and evolves.

Given that this project is simulating how minimal beginnings can generate complexity - inline with Oparin's suggestion [35] of an increasingly complex autonomous chemical system - it will be important to maintain a degree of integrity to how entities interact and how they produce new entities. The basis for the model will need to be a minimal population where each entity in the system represents a unique behaviour of interaction. As will be discussed in Chapter 2 a pre-existing model developed by James Crutchfield & Olaf Gornerup called the Finitary Process Soup [36] provides a useful starting point with one of the advantages of this model being that the entities are a special class of finite state transducer called ϵ-machines. These are minimal representations of unique physical processes that adhere to rigorous mathematical rules for their own construction and their collective behaviour and that can be quantified using measures of complexity [37]. In the words of Crutchfield & Gornerup their model allows a modeller to: "state the question of whether or not complexity has genuinely emerged over time in pre-biotic and pre-chemical processes" [36]. However their model has several limitations that needed to be addressed to allow this project's research aims to be pursued and this is discussed in the next chapter.

1.4 Scope

This research project is a computational study of the emergence and dynamics of proto-autopoietic systems as steady-state organisations that occur under various environmental conditions. The computer simulations that were performed focused on the nature of the interactions between entities and the basis for their self-organisation. The intent was not to accurately model the physical and chemical processes that lead to the formation of a proto-cell [38],[39] as an example of a complete autopoietic unit that satisfies Maturana & Varela's criteria. Instead the focus was on examining the emergence of proto-autopoietic networks from an initially uniform and unstructured state. The formation of a membrane/boundary - which is commonly demonstrated in other computational work on autopoiesis - was not a specific aim of this project. As discussed in Chapter 2 the necessity of a physical boundary for a system to become autopoietic is a contested issue and pursuing it risked de-focusing the main aim of this project which is on understanding the structures and processes that emerge from undefined beginnings. Furthermore the number of assumptions that would need to be designed into the model to support a physical boundary would need to increase significantly to ensure that a credible process of physical boundary formation could be accurately simulated. This was deemed to be an unnecessary complication that would detract from a more elegant, minimal model of an interacting population subject to environmental perturbations where the primary aim was to investigate self-organisation, adaptation and persistence[2].

Autocatalysis [40], and specifically autocatalytic networks, was not an explicit focus for this project. Autopoietic systems, even proto-autopoietic, are likely to consist of one or more autocatalytic cycles [33] and, in that context, they are examined. There is extensive literature on the formation and evolution of autocatalytic cycles [41] in origin of life scenarios but less so in the context of autopoietic systems. The key distinction in this project that distinguishes it from work on autocatalysis is the focus on the adaptive behaviour of the system in the presence of various forms of perturbation from the environment and neighbouring systems. This allowed the important cognition process of autopoietic theory to be explicitly examined alongside the autopoietic process of production and maintenance.

Other models of living systems were considered - Tibor Ganti's chemoton [42], Eigen & Schuster's hypercycles [43] - however as is discussed in the next chapter they assume the presence of reasonably sophisticated biochemical machinery such as information-encoded molecules that can control replicative processes. As should now be clear this project was

[2] I show that even a minimal model of interacting entities can demonstrate the emergence of boundary-like spatial patterns (see Chapter 7).

focused on examining the possible pathways *to* such biological capabilities and therefore, by definition, models that rely on templated replication were excluded as they did not support such research aims.

1.5 Outline of Chapters

Chapter 2 examines in detail the theory of autopoiesis and related literature. The structure of the first part of this chapter is based on the three criteria of an autopoietic as proposed by Francisco Varela [44]: self-boundary, self-maintenance and self-generation. This proves to be a useful framework within which to examine not just the theory, but also investigate the limitations and challenges to the underlying assumptions of the model. The main theoretical issue of whether or not an autopoietic system needs to have a physical boundary (i.e. an encapsulating membrane) or whether non-physical 'boundaries' are also allowed (e.g. a system is deemed to be maintaining a boundary if it is able to preserve its dynamic equilibrium) are discussed. Whilst the issue is not resolved here it does prompt the need to appropriately define the forms of organisation that are generated from my simulations. This is subsequently discussed and I propose the term *proto-autopoietic system* to describe a system that consists of dynamically stable strongly connected networks of mutually producing entities, that emerge under specific environmental conditions and that do not necessarily form a physical boundary. Previous computational work that has directly demonstrated autopoiesis (Varela et al. [9], McMullin [45]) or that has demonstrated behaviour indicative of proto-autopoiesis are discussed and compared and this gives particular attention to Fontana's algorithmic chemistry [46] and Crutchfield & Gornerup's Finitary Process Soup [36]. Comparison of these models concludes with the recognition that the Finitary Process Soup - albeit with limitations that would need to be addressed - provides a rigorous and credible foundation for examining self-organisation and to quantitatively measure any structural or network complexities that may arise.

Chapter 3 explains how the research aims were addressed by extending and enhancing the Finitary Process Soup model. Two models are introduced - the information niche model and the computation niche model - that were derived from the minimum number of assumptions required to generate sufficiently complex behaviour in an interacting population that was quantifiable. The information niche model extended the finitary process soup model [36] to examine the effect of environmental conditions and environmental perturbations on the dynamics of an interacting population. This model was called the information niche model to acknowledge the finding that the interacting population transformed itself to different structural configurations that fit to specific environmental conditions (i.e. analo-

gous to an ecological niche [47]) and that the information content of these different states could be quantified. The computation niche model enhanced the information niche model by formally defining a systems interface (analogous to a biological membrane) that was positioned between an internal interacting population and an environment. This membrane consisted of the same automaton types that were present in the internal population but with a different mode of operation e.g. whereas the automata in the internal population interacted to produce new automata, the automata in the membrane (so-called membrane automata) processed information from the environment and other membrane automata that may, or may not, trigger a membrane automaton to emit information that had the potential to excite or inhibit its equivalent automata in the interacting population. This proved to be a valuable enhancement as it allowed the autopoietic notions of structural coupling, cognition, and information processing to be examined. Analysis of this model revealed that the systems interface in conjunction with the environment and the internal population was computing the next state of the system. As such this model was called the computation niche model. Chapter 3 also describes the following methods that were used for analysing the simulation results: Shannon entropy [48]), structural complexity [37], interaction network complexity [36]) and network analysis measures such as determining the degree distribution [49] of a network. New methods for detecting strongly connected components of networks in an interacting population and testing those networks for dynamic stability were developed specifically for this project and these are also described.

Chapter 4 is a reproduction of my published paper, "Emergence and Dynamics of Self-Producing Information Niches as a Step Towards Pre-Evolutionary Organization" [50]. This paper describes the key properties of proto-autopoietic organisations that emerged from simulating a one-state automata population evolving under the influence of fixed and intermittent environmental conditions. The main contribution that this paper makes to the field of autopoiesis is that proto-autopoietic organisations emerge from simple beginnings, and that they have specific properties related to the structure of their interaction networks. They represent a minimal beginning for an autopoietic system. The paper introduces the notion of an information niche as a particular instance of a proto-autopoietic system as a dynamically stable strongly connected network of mutually producing automata that form distinct organisational steady states under various environmental conditions. Critically it is noted that information can be lost or gained during a perturbation and, in some cases, this leaves the system unable to transform itself back to a prior configuration state. The environment can play the role of adding the necessary information back into the population in the form of a perturbation which proves sufficient for the population to transform to prior states. The paper used the information niche model and also made use of most of the

information and network measures described in Chapter 3.

Chapter 5 describes the results of simulating a population of interacting two-state automata and examines the structure of the resultant steady-state populations. Simulation results reveal that competition between two niches (as separate proto-autopoietic systems) emerged and eventually led to an event where one of the niches came to dominate the population at the demise of the other niche. In the presence of some influx of automata from outside the population these previously competing niches that were operating on a 'competitive exclusion principle'[51] were now cohabiting in the population. New competitive behaviour in response to environmental changes were observed with the emergence of two competing survival strategies called 'replicate & lock-in' and 'mutual maintenance'. The structure and properties of the underlying networks that were partly driving such population dynamics were examined and this revealed similar properties to those that had been identified in the one-state information niche simulations (as per Chapter 4).

Chapter 6 examines the spatial patterns that emerged in one-state and two-state information niches under zero diffusivity conditions. In the one-state population the patterns that emerged under zero diffusivity conditions were characterised as two competing domains of automata separated by a dynamic and continually produced boundary consisting of two other types of automata. Competition between these domains proceeded under a 'protected outgrowth' mechanism determined by the expansion of the domain boundaries. The two-state niche also formed homogenous domains on the lattice consisting of a single type of automata that grew outwards until meeting other homogenous domains. However, there was no evidence of boundary-type automata. Instead the domains were in direct contact with other domains and competition between them proceeded by two mechanisms: 'replicate and lock-in' and 'mutual maintenance' with the former proving to be the more effective. The emergence of these various competitive, or survival, strategies were entirely unexpected and were not evident from examination of the individual automata.

Chapter 7 describes part one of a two part investigation into the cognitive process of an autopoietic system which was Maturana & Varela's concept for how an autopoietic system adapts to changes in its environment [7]. The ability of an information niche to assimilate and accommodate material that was generated from external processes allowing two niches (a one-state and a two-state niche) to interact and exchange material (i.e. automata) was simulated and the results are presented. There were two findings: (i) information niches that consisted of simpler entities tended to be more resilient in the presence of foreign automata, and (ii) they were also more readily reproduced in neighbouring populations. These observations suggest that proto-autopoietic systems that contain the simplest of automata should be more resilient to perturbations in the form of an influx of foreign

entities and, secondly, that simpler networks should be more easily reproduced. This has implications for understanding how autopoietic systems may scale and evolve.

Chapter 8 is part two of the investigation into the cognitive process of an autopoietic system. This chapter introduces the use of the computation niche model which explicitly defines the system interface of an autopoietic system with its environment. This allowed several features of autopoietic theory to be examined including: (a) structural coupling of the niche with its environment, (b) the relationship between a system interface (analogous to a membrane) and the production of new automata, and (c) the effect of environmental noise on interaction dynamics in the population. The main findings were that the system dynamics are hierarchical with an interplay of top-down, bottom-up and same-level information processing yielding a proto-autopoietic system that demonstrates information closure i.e. it is able to retain the information required to re-generate all possible system states; this was not evident from simulating the information niche model. This has implications for understanding the causal structure of an emergent proto-autopoietic system. An important finding was that proto-autopoietic systems with a population of automata that were too simple cannot respond effectively to extreme environmental conditions (specifically, the simplest of one-state automata ceased to participate in interactions with other automata). This observation implies that autopoietic systems may reside within a 'window of viability' [52], where they are not too simple nor too diverse, to endure under varying environmental conditions.

Chapter 9 presents the results of simulating the endogenous diversification of a computation niche driven entirely from an initial seed population. This seed population consisted of all 129 self-replicating automaton types that exist in one-state and two-state populations. These self-replicators were chosen as they could interact with each other to produce novel types of automata whilst also reproducing themselves. This was deemed to create a degree of competition between self-replication and the diversification of the population. From this the notion of whether novelty could be regulated via. self-organisation was examined. The results were unequivocal: an explosion in the appearance of novel automata was noted followed by a rapid tailing off in the rate of production of new types of automata. After 50 generations the population transitioned through four phases characterised as: I - Diversification, II - Competition, III - Penetration and IV - Saturation. The main finding was that open-ended novelty - even in the presence of a competing dynamic in the form of self-replicating automata - remained unregulated. There was no emergent regulation on the production of novel automata due to competition from established automata. Subsequently, the production of novel automata dominated population dynamics and this led to a diverse, unstructured population. Therefore one conclusion is that an ability to regulate the

rate of novelty production within a self-producing population could be a critical property of an autopoietic system. I believe this is a new finding in the field of autopoiesis and reinforces the notion that an autopoietic system must maintain itself within a 'window of viability'. Cognition could be the process by which the system maintains itself within a window of viability in response to changes in its own structure and changes to its external environment.

Chapter 10 discusses the results from Chapters 4-9 and evaluates them against the original research aims of the project. Several themes emerge in this chapter e.g. the notion of a proto-autopoietic or autopoietic system maintaining itself within a window of viability, that the information content of a self-producing system constrains or enables its ability to respond to environmental changes, and the emergence of strongly connected and hierarchical networks. These observations were drawn from an interacting population that was - at a fundamental level - driven by a process of competition occurring at the individual (automata), collective (network) and autopoietic (niche) level. It is proposed that the core dynamic of an autopoietic system arises from a competitive process, and that all other processes - such as structural transformations of the population in response to changes in the environment - are realised through competition at multiple levels. Not only does this have implications for what types of processes should be sought (i.e. competitive) in producing an autopoietic system in the real-world but this also has implications for bridging the conceptual gap between autopoiesis and Darwinian evolution i.e. selection at multiple levels (automata, network, niche) occurs in simulations of the most simple of autopoietic systems and therefore a competitive process is the continuum that joins these two theories. The general properties of an autopoietic system are also proposed as: (i) strongly connected networks that drive the self-production process; (ii) redundancy within that network and the population; (iii) diversity as a mechanism to recover from environmental perturbations; and (iv) modularity in the network architecture which equips an autopoietic system with the ability to completely reproduce itself. These properties provide the qualities of robustness and resilience which would be critical to the survival and long-term persistence of a simple self-producing system which can act as a springboard from which more complex forms of organisation could emerge.

Chapter 11 concludes with a summary of the research findings. The conclusion states that the hypothesis that autopoietic systems can emerge from simple, unstructured beginnings holds, and that the work undertaken in this project contributes to our understanding of the possible pathways to autopoietic systems. An assessment of the limitations of the research are described and these must be borne in mind when interpreting my results and conclusions. Recommendations for future work are also proposed.

CHAPTER 2

BACKGROUND AND LITERATURE REVIEW

This chapter provides the necessary background to understand autopoiesis as a model of a minimal living system. The three criteria for determining whether a system is autopoietic are examined in detail by reference to the current thinking and literature in the field. This leads into a review of computational models of autopoiesis (termed "computational autopoiesis") that are based on simulated artificial chemistries as a way to demonstrate how autopoietic systems can self-organise and endure. Several limitations in the field are identified, in particular the lack of any convincing narrative for how autopoietic systems may form from simple, unstructured beginnings.

2.1 A Minimal Living System

A living system is distinguished from non-living matter by its ability to reproduce and maintain itself [9]. To achieve this, a minimal living system must integrate three functions [4]: (i) it must maintain its identity through the localisation of its constituent parts (compartmentation); (ii) it must use free energy from its environment in order to maintain, grow and reproduce itself (metabolism); and (iii) it must be equipped with some form of heritable information that can be transferred to future reproductions of itself. Alexander Oparin proposed that the origin of the first living cell must have emerged from increasingly complex chemical reactions that were able to endure over extended periods of time [35]. This would be a form of autonomous chemical system able to demonstrate sufficient functionality and behaviour to be determined as living.

A biological cell is the archetype of a living system, and a minimally functional version is called a protocell [1]. Efforts to develop protocells have grown significantly in the past two decades [26] and experimental approaches have included both top down and bottom up methodologies[53]: (a) the top-down approach takes a contemporary biological cell with the aim of isolating the minimal genetic requirements to maintain the cell as a living system by the progressive removal of non-essential genes up to the point at which biological function is just retained [54], and (b) the bottom-up approach attempts to synthesise a biological cell from simple chemical precursors [55] such as nucleic acids and peptides contained within fatty-acid vesicles [56], peptide-nucleotide microdroplets as membrane-free protocells [57], or protein-polymer nano-conjugates [58]. Whilst the top-down approach efficiently makes use of the building blocks that already exist (DNA/RNA/proteins), it is not an approach that can directly explain how living systems may have emerged in the absence of such complex molecular machinery. By comparison, it is necessary with the bottom-up approach to consider more broadly the chemical pathways by which a protocell can be created.

A chemical pathway from an initially random assembly of molecules to a minimal protocell, without the use of any genetic apparatus, has been hypothesised [59] as feasible through mutually catalytic metabolic networks that exhibit the transfer of chemical information. Such assemblies of molecules would be held together by non-covalent interactions [60]. Whilst this is a compelling argument, there remains the issue of whether such assemblies of molecules have the capacity to store and transfer information and to undergo chemical selection and evolution in the absence of informational polymers [61]. Therefore, a major requirement is demonstrable proof that an assembly of molecules can retain and transfer information over generations in the absence of informational polymers such as RNA and DNA. There have been some suggestions of how this informational step could be achieved with the notion that protein interactions were “the first form of reproducing life and that nucleic acids evolved later as memory molecules” [62]. An alternative suggestion is that a protocell is the basic unit of prebiotic evolution [63] that increases in organisational complexity as it evolves. This implies that there are minimal cells (e.g. vesicles) that are sufficiently robust that they allow alternative phenotypes to be explored with successful variants representing a change in the functional capability of the protocell. Such successful phenotypes become the new basic unit of evolution from which more sophisticated phenotypes can be trialled. This is very much aligned to Oparin’s view of abiogenesis resulting from a long and increasingly complex system of chemical reactions.

Shirt-Ediss et al. [63] set out three challenges to experimental protocell research: (i) *coupling chemistry with vesicle dynamics*: discover simple reaction networks that can spontaneously absorb into existing vesicles to modify the properties of the vesicle to induce

growth and reproduction. In turn, the vesicle should be supportive of that chemistry (this has similarities to autopoiesis (see Section 2.2)); (ii) *finding conditions and mechanisms for minimal functional integration*: this requires a search for specific conditions and the set of interactions that lead to a minimally functioning system that, at the least, integrates spatial and kinetic mechanisms; and (iii) *characterising the evolutionary dynamics of pre-Darwinian protocells*: working with simple chemical structures to explore how such chemical assemblies could operate far-from-equilibrium in a robust manner such that a range of alternate phenotypes can be explored. Coupled to simple chemistry that can also divide with regularity, this may provide a minimal platform from which alternate mechanisms that produce increasingly reliable operation and heredity can be examined. As will be discussed in Section 2.2 Shirt-Ediss et al's third challenge resonates strongly with the notion of a proto-autopoietic system.

The investigative effort into exploring alternative chemical pathways to abiogenesis has given rise to a new discipline within the field of chemistry called systems chemistry that: "... seeks insight into complex networks of interacting molecules and their system-level properties. These properties emerge through the collective behaviour of the system's components and cannot be attributed to the individual components acting in isolation. The way in which specific interactions between the components propagate through the system dictates these emergent properties" [64].

This definition incorporates language from complexity science [34] (collective behaviour, emergent properties) and has parallels with the work of Maturana & Varela's theory of autopoiesis (see Section 2.2). Complexity science is the body of knowledge, tools and techniques for the study of complex systems which has been defined as: "A system in which large networks of components with no central control and simple rules of operation give rise to complex collective behaviour, sophisticated information processing, and adaptation via. learning or evolution" [34].

Complexity science is therefore concerned with how large systems change over time as a result of the interactions between the entities of which the system is composed [65]. Such relationships tend to be nonlinear, and interactions at the local level can lead to changes at the global level through a process of self-organisation [66]. A common phenomenon of self-organisation is the emergence of behaviour that cannot be predicted from examination of the individual entities of the system. This is one of the hallmarks of complex behaviour and, due to the nonlinear relationships involved, favours the use of mathematical models implemented as agent-based and/or numerical computer simulations to reproduce such dynamics.

There are two classes of computer model in systems chemistry:

1. Computational systems chemistry seeks to build highly detailed molecular simulations to accurately reproduce the physical and chemical kinetics that may be involved in the formation of a protocell [67]. Computational chemistry is an active area of research that requires access to substantial computer resources to perform very complex calculations such as interatomic forces and the electron density surrounding nuclei [68]

2. Abstract models that emphasise the general processes and properties that could lead to the emergence of systems that could support protocell formation. The common feature of such models is the focus on reproducing complex behaviour such as self-organisation, emergence and adaptation which are concepts that reside within the discipline of complexity science.

The field of complexity science - with its depth and richness of tools, concepts and methods that have been tried and tested across multiple disciplines - has the potential to enrich the domains of chemistry and systems chemistry [69]. The maturity, and therefore the usefulness, of complexity science, rather than systems chemistry, in developing our theoretical understanding of pathways to autopoiesis is more helpful. For example, the mention of networks and collective behaviour is similar to that used in the definition of systems chemistry. Whilst adaptation is implicit to the protocell as a "basic unit of evolution" [1], it is not covered at all in the definition of systems chemistry. Furthermore, whilst systems chemistry mentions "propagation" this is a rather ambiguous term and it is not obvious what information processing may mean in the context of a protocell. This is a serious omission given that information processing in living systems, and particularly biological cells, is an active and important field of investigation [70]. The complexity science description of a complex system is applicable to the concept of a protocell. In general complexity science has much to offer the development of the systems chemistry field, not least in bringing greater clarity and maturity of thinking to what constitutes a complex system. Whilst systems chemistry is fundamental to experimental protocell work it lacks the body of knowledge required to also examine the theoretical aspects of protocells. Therefore the main epistemological backdrop to this project is the language, concepts and tools of complexity science. This topic is returned to in Chapter 10.

Theoretical models of a minimal living system have been proposed with the three more prominent models referenced in protocell experimental research being Ganti's chemoton [42], Maturana & Varela's autopoietic systems [9], and Eigen & Schuster's hypercycles [43] [67] - see [39] and [71] for a detailed review of the state-of-the-art. Such models have guided and inspired the design of computer-based models [4],[8] to examine and explore the

dynamics and formation of *in silico* (artificial) cells. Two other important theories of living systems are (a) the Metabolism-Repair (M-R systems) model developed by Robert Rosen [72] and that overlaps considerably with autopoietic theory. M-R systems theory provides an important comparison to the adaptive nature of autopoietic systems and, as such, it is introduced and described in Section 2.2.3; and (b) Stuart Kauffman's autocatalytic sets [40] which explains how networks of reactions can become more complex over time. Whilst Kauffman's work isn't a complete theory it does provide important concepts that are relevant to thinking about pathways to living systems from simple beginnings. His work is most related to the specific process of autopoiesis and, as such, is discussed where it is most relevant (see Section 2.2).

Eigen & Schuster's hypercycle model [43] is an abstract model of self-replicating entities that form autocatalytic networks. They defined self-replication as the ability of an entity to catalyse its own reproduction. When that same entity formed part of an autocatalytic cycle, they referred to it as a network replicator and defined it as the dependency that an entity had on other entities to reproduce it. Self-replication is reminiscent of RNA, whilst network replication is characteristic of a metabolism. The combination of self-replicators and network replicators form a hypercycle. A hypercycle is a collection of entities that replicate themselves through self-reinforcing loops (self-replication) and that catalyse the production of other entities (network replication). In this way each entity catalyses the creation of the entities on which it is dependent for its own replication and with the final entity in such a system catalysing the first entity in a cyclical reaction. Therefore a hypercycle reinforces itself. Eigen & Schuster purport that this process of continual reinforcement through a system of replications satisfies the notion of a living system. As a theory it is wholly dependent on replicative processes that use informational molecules and highly refined catalysts (e.g. RNA and proteins) and, as such, can aid in both top down and bottom up experimental research that seeks to harness and/or reproduce modern molecular machinery. However, given that my research is examining minimal, unstructured beginnings of a living system, any theory that is dependent on the presence of complex molecular machinery is, by definition, outside of the scope of this project. Consequently Eigen & Schuster's hypercycle theory, whilst well-studied and supported, is excluded from further consideration.

Tibor Ganti proposed a particularly elegant model of a protocell which he termed a chemoton [73]. The chemoton is a contained system consisting of three reaction cycles: an autocatalytic cycle that constitutes the protocell's metabolic system, a replication cycle consisting of the protocell's genetic system, and a membrane-forming system (see Figure 2.1). Nutrients enter the cell and waste is extracted from the cell and this process is

managed by the metabolic system. The creation, maintenance and reproduction of the cell is the result of a carefully orchestrated interplay of these three subsystems. The chemoton model is an intricate and detailed explanation of the internal features of cellular life that continues to prove its worth as a general heuristic for experimental design [74].

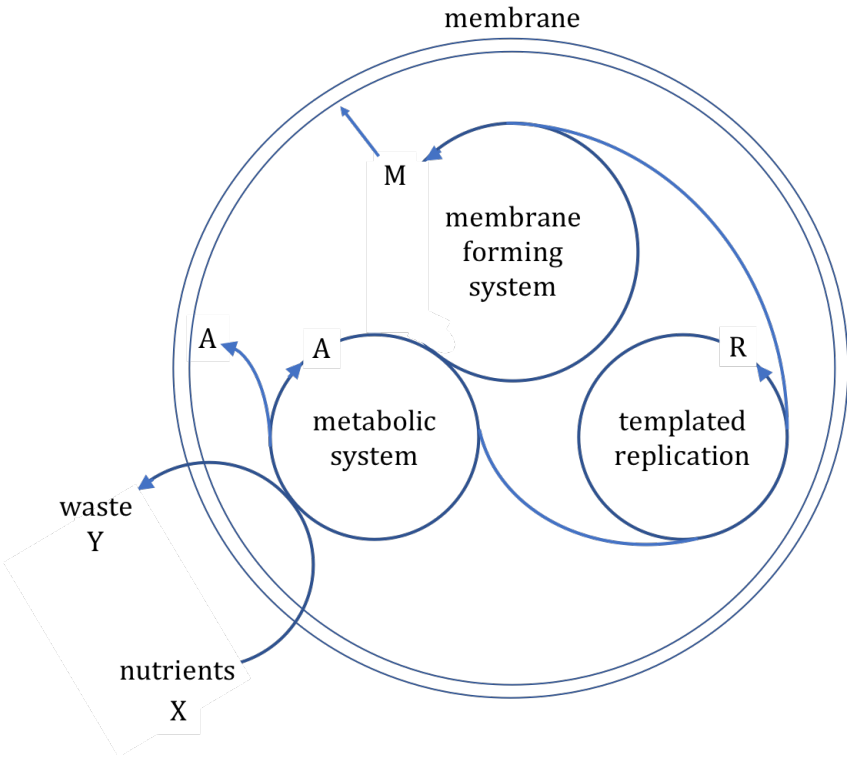

Figure 2.1: The metabolic cycle of Ganti's chemoton [42] is an autocatalytic chemical cycle consuming the nutrient 'X' and producing 'Y' as waste with intermediate 'A'; 'R' is a by-product of the replication process that is required to produce 'M' the membrane molecule. Adapted from [42].

Ganti's chemoton offers a simpler depiction of the necessary processes to generate and maintain a minimal living system that also includes a templated replication process, albeit Ganti is less prescriptive over the use of informational molecules. The chemoton model represents a bottom-up constructive approach. However, whilst this level of detail builds confidence in the model, it has been argued that it is too prescriptive and, as such, the chemoton model is too narrow to expand to include higher notions of life centred around concepts of epistemology, cognition and social behaviours [8]. By comparison the theory of autopoiesis does not have such profound limitations.

Maturana & Varela's theory of autopoiesis is a more general theory of a living system that does not require the explicit processes of templated replication nor informational

molecules. Autopoiesis is the preferred conceptual framework for bottom-up protocell researchers looking to understand the system logic of a minimal living cell [26]. The openly cited reason for the continued popularity of autopoietic theory in the protocell researcher community is its independence from nucleic acids thus providing researchers with greater freedom in how they design their experiments [8].

There are a number of other related models of living systems including Beer's Model of Living Systems [75], Schwarz's Living System Model [76], Dittrich & di Speroni's chemical organisation theory [77]. These models are only cited here for completeness; conceptually they are more detailed, more prescriptive about the processes that are required and draw on a larger number of assumptions. Therefore they are not minimal models of living systems and are not considered further. Figure 2.2 provides a summary of the core literature on autopoiesis and related works.

2.2 Autopoiesis

In 1974 two Chilean biologists, Humberto Maturana and Francisco Varela, announced their theory of how living systems are organised. They proposed that all living systems are self-producing - *autopoietic* (*auto* for self and *poiesis* for production) - and that it is this unique behaviour that distinguishes living from non-living matter. Figure 2.3 illustrates the concept of an autopoietic system as a topological bounded structure maintained by the dynamic interplay between a boundary and internal reactions. As can be seen, the semi-permeable boundary allows the substrate A to diffuse into the system where it participates in the internal reaction $A \rightarrow S$ the product of which is a component of the boundary itself. Over time the component S decays to a waste product P in the reaction $S \rightarrow P$ leaving a hole in the boundary. This hole is subsequently repaired by the migration of the product S to the boundary thus completing a maintenance cycle. This minimal example is demonstrating that: "A system can be said to be living if it is able to transform external matter/energy into an internal process of self-maintenance and production of its own components" [8].

A protocell - as the archetype of autopoiesis - is an open, dissipative system with a sequence of chemical processes occurring inside the cell to maintain a boundary and therefore its identity within its environment. The maintenance of its boundary and its identity is the defining behaviour of an autopoietic system.

An autopoietic system is able to maintain itself through its internal network of reactions that produce the components of which the system is composed. Therefore, autopoietic systems: "(i) through their interactions and transformations continuously regenerate and

	Theory of Autopoiesis	Computational Autopoiesis	Related Work
1950-1980	Realization of the Living (Maturana & Varela 1973) [9]	Computational model of autopoiesis (Varela et al. 1974)[9]	Cybernetics (Ashby 1956) [168] Viable System Model (Beer 1959) [75] M-R Systems (Rosen 1970) [72] The Chemoton (Ganti 1971) [73] Hypercycles (Eigen & Schuster 1979) [43]
1980-2000	Formal Model of Autopoiesis (Zeleny 1981) [10] Autopoiesis, reproduction, heredity & evolution (Maturana & Varela 1987) [32] Autopoiesis – Implications & Applications (Mingers 1990) [88]	Rediscovering computational autopoiesis (McMullin & Varela 1997) [45] Evolving Reaction-Diffusion Ecosystems with Self-Assembling Structures in Thin Films (Breyer et al. 1998) [113] Matrix Chemistry (Banzhaf 1999) [90] Lattice Artificial Chemistry (Ono & Ikegami 2000) [114]	Algorithmic Chemistry (Fontana 1981) [46] Collective Autocatalysis (Kauffman 1984) [40] GARD model (Segre et al. 1996) [104] Viable System Theory (Schwarz 1997)[76]
2000-2018	Minimal Model of an Autopoietic Cell (Luisi 2003) [6] Autopoietic and (M,R) Systems (Letelier 2003) [92] Autopoiesis and Natural Drift (Etxeberria 2004) [29] Autopoiesis With and Without Cognition (Bitbol & Luisi 2004) [12] Autopoiesis 40 years later (Razeto-Barry 2012) [15] Systems of Creation (Mann 2012) [2]	30 Years of Computational Autopoiesis (McMullin 2004) [112] Autopoiesis and the Game of Life (Beer 2004) [115] Autopoiesis and Cognition with Tesselation Algorithm (Bourgine & Stewart 2004) [13] Autopoietic Automata (Wiedermann 2007) [116] Simulation of an Abstract Autopoietic Machine (De Loor et al. 2009) [117] Anticipatory Artificial Autopoiesis (Dubois & Holmberg 2010) [93] Lattice Model of Emergence and Maintenance Autopoiesis (Wang et al. 2013) [118] Evolutionary Simulations of Autopoietic Cells with Cognition (Matsufuji & Narikiyo 2015) [119]	Autonomy and Open-Ended Evolution (Ruiz-Marazo 2004) [71] Chemical Organisation Theory (Dittrich 2006) [77] Finitary Process Soup (Crutchfield & Gornerup 2006) [36] Characteristics of reflexive, autocatalytic networks (Hordijk et al. 2010) [41] Energy Minimisation Model (Friston 2013) [93]

Figure 2.2: Summary of the key papers contributing to or closely related to the field of autopoiesis.

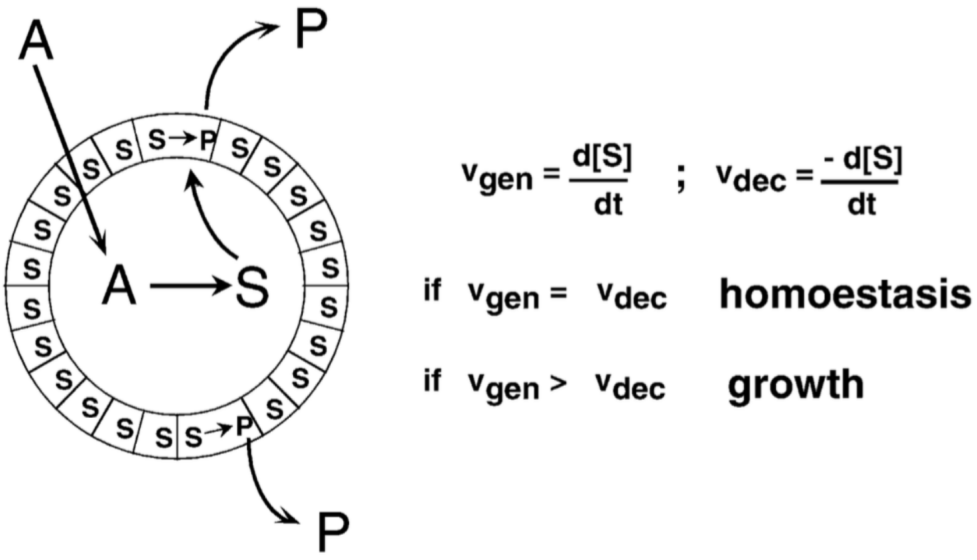

Figure 2.3: Luisi's schematic of a minimal autopoietic cell where a substrate entity (A) produces the product (S) which links to other S entities to form a boundary which encapsulates the $A \rightarrow S$ reaction. Over time S decays to the waste product (P) leaving a hole in the boundary which is repaired by a newly produced S migrating to the cell boundary. The dynamic behaviour of the system is described by the two differential equations $v_{gen} = \frac{dS}{dt}$, $v_{dec} = \frac{-dS}{dt}$ and the interplay of the two determines the present state of the autopoietic cell as growing, at homeostasis, or decaying. Taken from [8].

realize the network of processes that produced them" and "(ii) constitute [the cell] as a concrete unity in space in which [the components] exist by specifying the topological domain of its realization as such a network" [9]. In other words the autopoietic system organises the production of its own components which allow it to maintain the network that is producing them. The self-referential nature of these systems is a signature characteristic of autopoiesis. Consider Maturana's own words on this matter:

"When you regard a living system you always find a network of processes or molecules that interact in such a way as to produce the very network that produced them and that determine its boundary. Such a network I call autopoietic. Whenever you encounter a network whose operations eventually produce itself as a result, you are facing an autopoietic system. It produces itself. The system is open to the input of matter but closed with regard to the dynamics of the relations that generate it" (taken from [78]).

Luisi [8] offers a useful depiction of his "cyclic logic of cellular life" (see Figure 2.4). This has proved to be a useful framework within which to understand and organise my own results on simulating the formation of autopoietic systems (see Chapter 4).

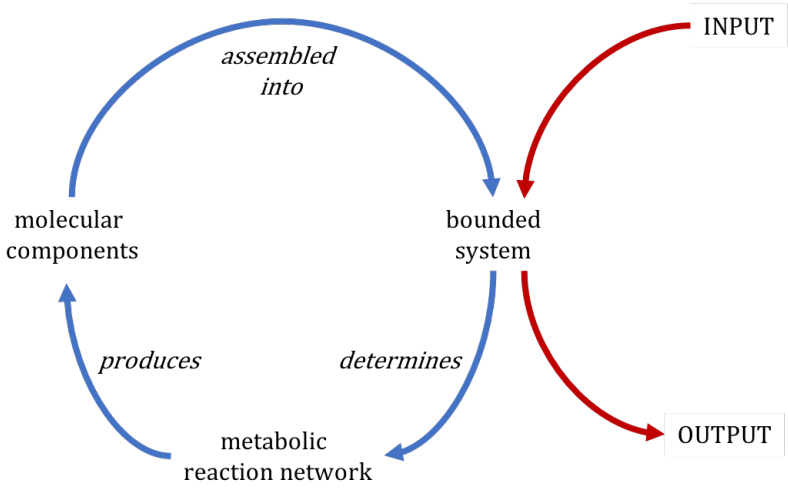

Figure 2.4: An autopoietic system depicted as Luisi's cyclic logic of cellular life [8]. Adapted from [8].

For me the most compelling aspect of autopoiesis - and as illustrated in Luisi's cyclic logic diagram - is that it does not require any assumptions about the specific molecules or chemistries that are required to construct a living system.

Francisco Varela (from [8]) proposed three criteria for autopoiesis:

Component	**Criteria**
Self-boundary	Does the system have a boundary of its own making?
Self-maintenance	Is the system capable of maintaining its own identity through dynamic processes? Are the components that are being used up being made anew by the system itself?
Self-generation	Does this happen throughout a network of reactions that are generated by the system itself?

Table 2.1: Varela's criteria for autopoiesis [8].

Applying these criteria to the real world, Luisi gives the example of the following as not being autopoietic: "a virus.... as it does not produce the protein coat of its boundary or its nucleic acids (the host cell does this)" [8]. Each of these criteria will now be described along with related literature.

2.2.1 The boundary of an autopoietic system

Applying the first criteria - the system has a boundary of its own making - is perhaps the most contentious issue. As explained by Barry McMullin, with molecular autopoiesis (i.e. as it pertains to a biological cell), "the boundary performs at least the function of limiting

or controlling the spatial diffusion of the molecules constituting the system" and "in the absence of such control on diffusion, the reactant concentrations may dilute to the point where one or more of the defining reactions effectively ceases to operate, and the whole self-sustaining reaction network then breaks down" [33]. In other words, molecular autopoiesis is wholly a physical manifestation of an autopoietic system and the criteria should apply to a physical system. However, and McMullin goes on to explain, a computer simulation of an autopoietic system (see Section 2.3) demonstrates the compartmentation of a reaction network with the compartmental boundary maintained by that network. In the simulation the boundary is constantly decaying and that requires continuous maintenance which is a sufficient demonstration of one of the phenomena of autopoietic systems. Nevertheless, and as explained by McMullin, "... the fact that the spatial localization is regularly interrupted in this way makes it more difficult to be clear what exactly the 'topological' autopoietic requirement is" [33]. Here McMullin is referring to an older criterion of an autopoietic system as "specifying the topological domain of its realization" [7] which Varela subsequently simplified to "does the system have a boundary of its own making?" [9]. The apparent quandary that McMullin identifies is born out of his investigation into what distinguishes an autopoietic system from an autocatalytic one. This is an important question as, it is generally assumed, that any reaction network that continually produces the components that regenerates the network is an autocatalytic one. An autopoietic system is highly likely to always consist of an autocatalytic reaction network. What, then, is the distinction? As McMullin states, "the critical distinction is that autopoiesis specifically requires that this confinement should itself be in some sense a product of the confined reaction network, whereas collective autocatalysis is assumed to rely on some independent confinement mechanism" [33]. Dissatisfied with the lack of clarity of Maturana & Varela's criterion McMullin proposed the following informal heuristic test [33]:

1. Consider two instances of the same collectively self-sustaining reaction network consisting of exactly the same set of molecular species

2. Each is constituted instantaneously by distinct collections of individual molecules occurring in separate reaction vessels

3. Mix the contents of the two vessels together into a single vessel assuming that any food set continues to be available

4. Are there still two separate reaction networks or just one?

Statement 4 is only true if the networks themselves maintain their individuality in the absence of any spatial separation mechanism. If this can be meaningfully shown then the reaction networks can be reasonably believed to meet the criteria for "specifying the topological domain of its realization" [33]. If the reaction networks cannot be readily distinguished then the singular network that is the product of their amalgamation should be considered as collectively autocatalytic. I acknowledge what McMullin is attempting here - to generalise on the concept of a boundary to extend the applicability of autopoietic theory outside of cellular life - however how does one use this in practice? How does one go about distinguishing the continued co-existence of two separate reaction networks that are constituted of an identical set of molecules? This requires an ability for the reaction networks to co-exist in a physical space that would, nevertheless, allow them to maintain themselves as separately identifiable entities. Indeed, McMullin goes on to use his heuristic test on contemporary state-of-the-art computer simulations that may demonstrate autopoiesis [33] and these included: Walter Fontana's algorithmic chemistry which I discuss in Section 2.3.2; John Holland's α-universes [79]; Tom Ray's Tierra model [80]; and the Substrate-Catalyst-Link (SCL) model [9] which McMullin developed with Francisco Varela and which I present in Section 2.3.1. Given that three of these models do not specifically set out to demonstrate autopoiesis - they allude to the existence of a relationship based on observations of self-organisation, renewal and persistence - it is of no great surprise that McMullin's "heuristic test" places them firmly as collectively autocatalytic systems and not autopoietic. However, what is surprising is that the SCL model, designed as it was to specifically demonstrate autopoiesis, does not in fact pass the McMullin heuristic either and therefore should not qualify as exhibiting *proper* autopoietic organisation. The emphasis here on *proper* is mine, and in recognition of the contested status of what is deemed an irrevocable characteristic of autopoietic behaviour. It is interesting to note that the majority of discussion in the literature centres on the definition of what qualifies as an autopoietic system rather than on a deeper understanding of the underlying mechanics from which self-producing behaviour emerges. One of the contributions that my work makes here is to bring a quantitative dimension to the underlying processes and components that constitute a system-level behaviour that demonstrates how a system can maintain its identity within a changing environment and, it can be argued, is maintaining a non-physical boundary.

An attempt to illuminate the mechanics of an autopoietic system comes from the field of artificial life [81] [1] where Virgo et al [16] challenge the significance (or not) of the spatial boundary in an autopoietic system and, in doing so, deconstruct the continual renewal of such systems to processes and dynamics. They agree that boundary formation and

[1] Incidentally it has been suggested that autopoiesis is a founding concept for artificial life.

maintenance is critical to the demarcation of the living system as a unity against its background environment, however, the boundary does not exclusively take on the role of containing the processes that constitute the autopoietic system. In separating out demarcation from containment the authors de-conflict two concepts which, they claim, are too often conflated: the physical boundary of an autopoietic system and the operational limits of the system itself. The former is produced by the system whilst the latter determines which processes are part of the system. Their aim is to bring precision to the definitions and meaning associated with autopoiesis. For example, they define a process as, "something that happens repeatedly or which tends to happen whenever the right conditions are met" [16] and that within the physical/chemical realm that such processes share properties e.g. every process transforms something into something else. Processes have a causal effect. By comparison, the dynamics of a system are the way in which the variables of the system change over time and processes are the things that effect those changes. The essential point here is the co-dependence between processes (e.g. process B is wholly dependent on process A) and that this forms networks of dependent processes which have the property of operational closure. Operational limits therefore describe which processes are in scope to the correct functioning of an autopoietic system. Consider Figure 2.5, which illustrates an autopoietic system that consists of several inter-dependent processes one of which ('M') forms the boundary. One of the enabling processes on which process 'M' is indirectly dependent (process 'W' in the example) resides outside of the operational limits.

From Figure 2.5 the processes 'w','x','y' and 'z' are not part of an operationally closed network and there is an absence of cyclical dependency between them. By comparison, the processes 'a','b','c' and 'M' are in a strongly connected network that is cyclical and operationally closed. One can assume, and Virgo et al's depiction does not dissuade us otherwise, that those processes which reside within the operational limits are also contained within the spatial boundary formed by process 'M'. As Virgo et al. state quite clearly the spatial boundary of an autopoietic system is not the same as its operational limits. This is an interesting claim as, apart from challenging the conceptual constraint that an autopoietic unit must have a physical boundary, it clarifies the embedded nature of an autopoietic system in its environment. For example, by accepting that the spatial boundary of an organism is not equivalent to the operational limits of the system, this forces an acceptance that an autopoietic system may include processes that are not occurring within its spatial boundary. This is a pertinent point to bear in mind when considering the role of structural coupling in the process of cognition within an autopoietic system (see Section 2.2.3). They then proceed to prove this statement by referring to the original works of Maturana & Varela where they state that autopoietic systems are homeostatic. They test this statement

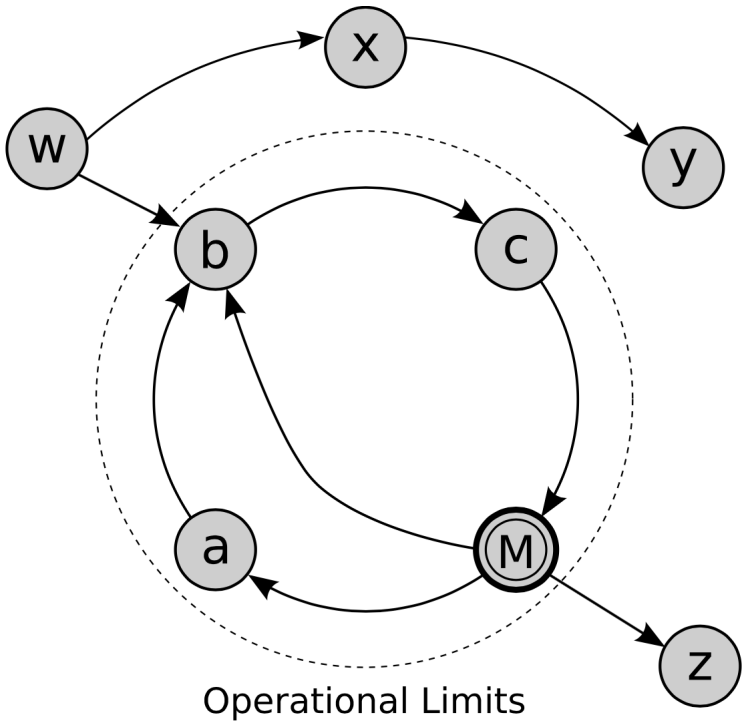

Figure 2.5: An illustration of the operational limits of an autopoietic system as suggested by Virgo et al [16]. Taken from [16].

by demonstrating that homeostatic machines can consist of processes and dependencies outside of the defined operational limits of the autopoietic unit e.g. a thermostat as a homeostatic machine has to take into account the heater, the air in the room, and so on.

This notion of dependent processes that reside outside of the classically defined autopoietic unit they refer to as "extended autopoiesis" [16]. To illustrate this point Virgo et al. recite the example given by Wheeler [82] of an earthworm: the worm builds tunnels held open by its secretions which in turn helps it to digest its food. If the autopoietic boundary of the worm is considered as stopping at its outer skin then this completely ignores the dependency that it - as an autopoietic system - has on the effects of its secretions. So what is the autopoietic system here? The worm or the worm and its secretions and tunnels? Maturana & Varela themselves provide the explanation, “... if one says that there is a machine *M*, in which there is a feedback loop through the environment so that the effects of its output affect its input, one is in fact talking about a larger machine *M'* which includes the environment and the feedback loop in its defining organization” [7]. Therefore the worm and its secretions form the autopoietic system even though the secretions reside outside of the physical spatial boundary of the worm itself. In conclusion, Virgo et al. have

demonstrated a respectable argument for why defining the spatial boundary as a critical defining component of an autopoietic system is too limited and risks missing important structural dependencies. Their work also appears to highlight a contradiction in Maturana & Varela's original thinking between the necessity of a boundary to achieve operational closure whilst paradoxically also recognising that dependencies on processes external to that boundary should be considered part of the operational closure of the system. Virgo et al. set out to challenge the notion of the sacredness of a spatial boundary in identifying autopoietic systems and I believe they do this well through the notion of extended autopoiesis. This does, of course, raise the question of how to identify autopoietic systems if spatial boundaries are not a reliable guide. Surprisingly they do not explore this and yet they have laid out the necessary concepts - dependent processes and extended autopoiesis - from which a procedure could be developed to detect and trace the autopoietic forms in a complex system. My work progresses these concepts somewhat with an investigation into the processes and dynamics that lead to the formation of non-trivial self-producing populations of interacting entities. As will be discussed shortly, I claim that such interacting populations that have evolved to a steady-state configuration under specific environmental conditions - what I call a niche - are proto-autopoietic. I introduce the term proto-autopoietic here to refer to those critical processes that generate a self-producing system capable of reaching a dynamic equilibrium, but that do not necessarily form a physical boundary.

Another challenge to Maturana & Varela's insistence that the boundary is a physical one comes from the social sciences. Niklas Luhmann was the pioneer of social autopoiesis [18] and who quite successfully introduced the concept of autopoiesis into efforts to understand collective human behaviour. He stated his goal as, "the application of the notion of autopoiesis to social systems [which] required the development of a more general 'non-physical' notion of autopoiesis" (from Vanderstraeten's review [83]). Luhmann began to tackle this by proposing that the social processes of the autopoietic network were processes of communication between people rather than molecular reactions. In Luhmann's own words: "For a theory of autopoietic systems, only communication is a serious candidate for the position of the elementary unit of the basic self-referential process of social systems" [18].

Luhmann's adaptation retains the main feature of autopoiesis - self-maintenance due to a process of self-generation from within - and that the boundary in a social system are the rules that define the system. These social systems are open in that they interact with their immediate environment and other social systems, and they do so without losing their identity. Consider a football team which occupies a location (the football ground), the team colours, the team emblem, the team's history and its supporters. These define the properties

of the system and new players and new supporters are transformed into being team players and team supporters as they become integrated into the bounded structure which is the team's identity. Consider Figure 2.6 which is reproduced from [8] and illustrates the same cyclical logic that Luisi [8] uses to define an autopoietic system (as per Figure 2.4), except that here human relationships substitute for chemical reactions and the rules of the social community substitute for the membrane boundary. The critical distinction that Luhmann made and that extricated autopoiesis from the biological realm - sadly without the support of Maturana & Varela - was to re-define a boundary as non-physical. This was an important development in the field of autopoiesis that led to application of the theory into other non-biological areas such as art [19], knowledge in institutions [20], computation theory [21], information systems [22], law [23] and architecture [24]. As will be seen in later chapters physical and non-physical boundaries are evident in my work, which suggests that Maturana & Varela's prescription for a physical, bounded domain may be too restrictive and that challenges to their original work have merit.

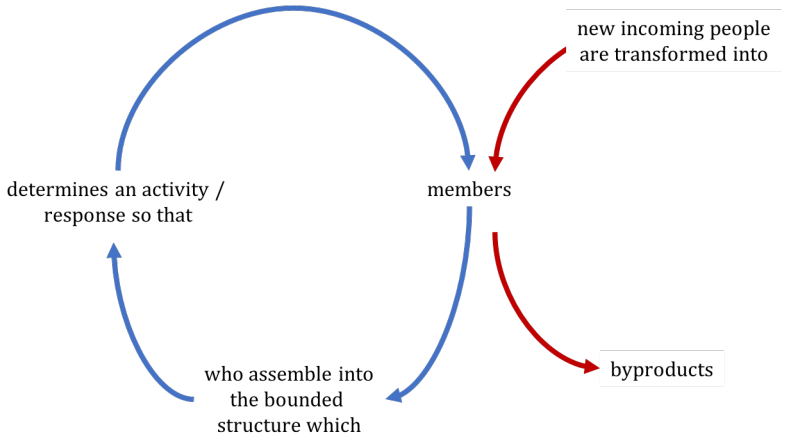

Figure 2.6: The concept of social autopoiesis retains the circularity of chemical autopoiesis except that people are the entities that enter and leave the autopoietic system and the interactions between them are in the form of communication. Adapted from [8].

The final challenge to the physical boundary conjecture comes from the field of synthetic biology and protocell research. Whilst some high profile protocell researchers specifically denote the need for a membrane [55], there is a growing body of research focused on membraneless protocells [84],[85],[86]. These approaches employ complex coacervates formed from aqueous two-phase separation techniques (such as electrostatics) [84]. If we consider the two-phase separation that occurs when oil and water are mixed together, then coacervate protocells employ the same principle, but entirely in an aqueous solution, by varying the pH, temperature and ionic strength of the two components with separation

occurring when the polymer component exceeds a given threshold [87]. So does this mean that biologists are abandoning autopoiesis as a systematic framework? I believe the answer is no they are not, and instead greater emphasis is being placed on the organisational logic of a cell as consisting of autopoietic processes [2] that do not explicitly demand the formation of a physical boundary (see Figure 2.7). The protocell is considered as an organised chemical system that undergoes changes according to its own activity and the inputs that it receives from its environment. Of course, this requires some delineation of what is part of the system and what is external to it; however that particular task is left to the individual researcher to define within the context of their own experiments.

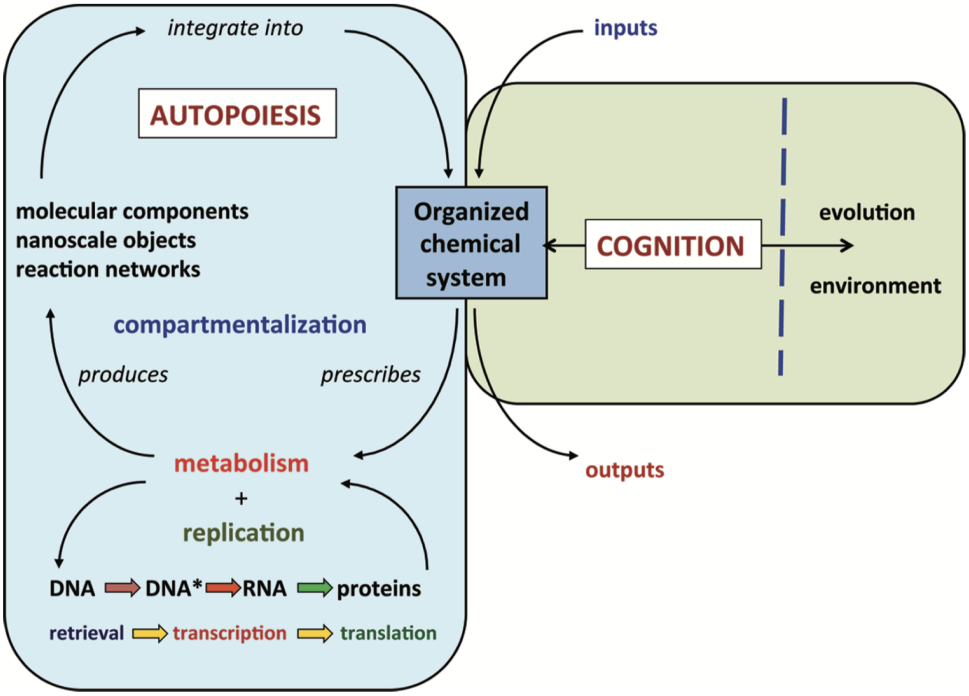

Figure 2.7: The organisational logic of modern cellular systems as proposed by Stephen Mann [2] that is an adaptation of Luisi's cyclical model of cellular life. Taken from [2].

In summary, the boundary of an autopoietic system is considered a critical criterion by the founders of the theory (Maturana & Varela) and yet it is considered a contested issue. Two competing notions continue to exist in the literature: those who adhere to the strict physical meaning of a membrane-like boundary that only makes sense within biological systems; and those that promote a broader meaning of boundary to denote the existence of cyclical processes that are operationally closed with the effect of maintaining the identity of the system. The former advocate that only physical boundaries that encapsulate the

reactions that create the boundary itself qualify as autopoietic systems. The latter advocate that the original physical meaning of a boundary is too restrictive and excludes a broader understanding of so-called extended autopoiesis [16] where dependencies outside of any physical boundary are still critical to the functioning of that autopoietic system. The contribution that my research makes to this discussion is threefold: (i) I demonstrate that physical membrane-like boundaries can form spontaneously in very simple populations driven entirely by the chemical affinity between interacting entities; (ii) that the identity of a self-producing and self-sustaining population of interacting entities can persist even under significant environmental perturbations *in the absence of a physical boundary*; and (iii) given that I observed the emergence of physical and non-physical boundaries in my simulations, this suggests that the notion of "extended autopoiesis" may well be correct. In general terms my work provides additional insight into the underlying dependent processes, structures and properties that lead to the retainment of a system identity. As discussed in Chapter 10, I outline the properties that I have observed in studying the proto-autopoietic networks that provide a resilient mechanism for maintaining system identities. I also offer the rule that a system is autopoietic if it can maintain sufficient information within its dynamic organisation to re-generate and maintain itself even after severe environmental shocks. The interesting observation that arises from this is that in some cases a system is wholly dependent on the environment to provide the necessary information required for it to re-generate itself. This strengthens the case for the extended autopoiesis argument. From my own research I find that I associate my understanding closer to that offered by Bourgine & Stewart where “an autopoietic system is a network of processes that produces the components that reproduce the network, and that also regulates the boundary conditions necessary for its ongoing existence as a network” [13].

2.2.2 Maintenance of an autopoietic system

Maintenance - within the context of autopoietic theory - is the continued and enduring presence of the overall organisation of the system. Maturana & Varela give a very specific meaning to organisation as, “... those relations that must be present in order for something to exist” (p. 42, [32]). The organisation of an autopoietic system is the relation between its components and the properties of those components that define the system as a single entity (a unity). For example, the organisation of a computer can be described as the necessary relations between components such as the central processing unit, memory, hard drives, power supply and so on. The unity of these components may be identified as a computer as this organisational form would produce the necessary properties expected of a computer.

Organisation is the invariant property of an autopoietic system in that if the organisation changes then the identity of the system changes (e.g. removal of the central processing unit in our computer means that it is no longer identified as a computer) and may no longer be autopoietic. Maintenance is about the continued renewal of those components that are required to maintain the functional relations that permit the system to acquire and regenerate its own identity. Such maintenance represents organisational (or operational) closure whereby the product of the organisation of the system is the organisation itself. This is the essential and distinguishing behaviour of autopoietic systems from other autonomous systems. All possible states of the system must maintain this autopoietic organisation otherwise the whole system falls apart.

Whilst the organisation of a system describes the invariant properties of the system, its structure are those variable elements that actually constitute the system as a unity in space and time. Whilst the organisation of a protocell does not change between different manifestations of the cell (they are all of the same organisation which constitutes their autopoietic behaviour), their structures will be different. Structure describes the actual components and the actual relations of an autopoietic system. Structure is the real manifestation of an autopoietic system whilst its organisation is the more abstract generality that is common to all possible manifestations of such a system. An autopoietic system is structurally determined i.e. the structural changes that are possible within the system at a moment in time are determined by the current structure of the system itself. Structural changes arise through endogenous and exogenous sources as described by John Mingers [88]: "... [structural changes] will occur in response to both internal dynamics and environmental interactions.... perturbations in the environment trigger changes of state in the organism, but since all possible changes must maintain autopoiesis, the actual nature of these changes and the possible interactions which an organism can successfully undergo are determined by the organism's physical structure".

The relevant point here is that the environment does not determine or specify the structural changes that occur in an autopoietic system. Only the present structure of the autopoietic system can determine what the possible state changes to the system are. Environmental perturbations can only act to trigger structural change and they do not determine the nature of that change. The interplay between environment and autopoietic unit, with the structure of the latter being influenced by the former, is known as structural coupling and this is discussed in Section 2.2.3.

An autopoietic system - a unity - has both organisation and structure. Such a unity is realised at a moment in time as a particular structure and the changes in state of the system are structurally determined. There are many possible structures which can realise

the same organisation in a many-to-one relationship. The structure will have properties and features not specified by the organisation e.g. the particular brand of CPU in the computer, the storage capacity of the hard disk, and so on. Hence, structural changes occur without altering the organisation e.g. as our hypothetical computer ages we upgrade the processor, add more memory, replace the power supply and yet its identity as a computer remains unchanged. However, organisation and structure are not independent of each other. An organisation of a living system can only exist (i.e. its identity) through the continued renewal of its components with the ability to do that, from moment to moment, determined by the structure of the system. These are inextricably linked concepts. The operational limits of autopoietic systems are defined by its organisation and its relationship with its environment. The notion of extended autopoiesis that is implied here is relevant to the exploration of the possible pathways to autopoiesis and, more specifically, the types of organisation that may unfold from simple and uniform beginnings.

The notion of organisation and structure as two separate but linked entities is reinforced by Robert Rosen and his Metabolism-Repair (M,R) theory [72]. Rosen (who was a pioneer of studying biology as a complex adaptive system) claimed that the organisation of a system must be independent from the "material particles" [2] that constitute the system. In a story told by his daughter Ms. Judith Rosen, he explains this quite beautifully [89]: “The human body completely changes the matter it is made of roughly every 8 weeks, through metabolism, replication and repair. Yet, you’re still you with all your memories, your personality... If science insists on chasing particles, they will follow them right through an organism and miss the organism entirely”.

Like Maturana & Varela, Rosen is emphasising the importance of understanding the organisation of a living thing rather than what it is made of. This is partly a statement that reductionism is not sufficient to understand biological phenomena and also an indication of what Rosen believed, namely, that understanding the relations between things in a living system is more important to explaining a living system than understanding the individual parts of that system.

Robert Rosen’s Metabolism-Repair theory is based on the notion that biological systems are distinguished from non-living systems by their organisation, which is a result of the complex interactions between the components of the organism, the behaviour of which cannot be reduced to any one component in isolation. Specifically, “when we break the system apart in order to study it, we destroy its organization and therefore cannot see how it functions” (Robert Rosen as quoted in p. 118 of [90]). His concept of organisation is that, “... a system is organised if it autonomously tends to an organized state” [91] through a

[2] Rosen’s "material particles" are synonymous with Maturana & Varela’s "structure".

thermodynamic process of self-organisation. The link to thermodynamics and, specifically the Second Law of Thermodynamics, would therefore suggest that such organised states are out of equilibrium and that the underlying processes of the system are open and dissipative. Rosen suggests that the measure of a system's degree of organisation is equivalent to the improbability of its state (although he does not offer a method for determining this). From this he suggests that identifying and studying the properties of organisations that are able to autonomously move to an organised state should be our primary focus in understanding biological systems. This motivation led to his development of the Metabolism-Repair (M,R) system theory that attempts to capture the minimal functionality of a living system.

An (M,R)-system consists of two functions: Metabolism (M) which is an abstraction of anabolic and catabolic functions, and Repair (R) which is an abstraction of a genetic function that provides the information necessary to construct the M-R system (including re-generation and replication). Unlike Maturana & Varela, Rosen does not specify the need for a boundary and in this sense it is a more general formalism of an autonomous, self-producing system. Consider Figure 2.8 which illustrates an (M,R) system as consisting of A an environment, B a Repair function, f a Metabolism function and Φ a Replication function. The diagram can be understood as follows: A is transformed into B assisted by f, B is transformed into f assisted by Φ, f is transformed into Φ assisted by B. Here the dashed and solid lines denote the efficient cause (the process which brings something about which, in chemical terms, would be a catalyst) and the material cause (the physical properties that are being changed in the formation of something i.e. chemical transformation) respectively, with the directional arrows indicating the flow of causation. Metabolism is the set of chemical transformations $A \rightarrow B$ catalysed by a set of catalysts f. Repair is the production of the set of catalysts f as instigated by the growth and decay of the system catalysed by the replication system Φ. The organisational invariance (which Rosen calls Replication) is realised through the maintenance of the repair system. In the (M,R)-system model all catalysts are produced internally.

From this Rosen proposes that, "... a material system is an organism if, and only if, it is closed to efficient causation" (p. of [91]). That is, if f is any component of such a system, the question "why f" has an answer within the system, which corresponds to the category of efficient cause of f' (p. 244 of [91]). In simpler terms, all information required about the system and its environment must be encoded into the organisation of the system itself. This information is "capable of acting causally on the organism's present behaviour based on relations projected to be applicable in the future" [92]. This insight gave rise to the notion of (M,R)-systems as anticipatory: "An anticipatory system is a natural system that contains an internal predictive model of itself and of its environment, which allows it to change state

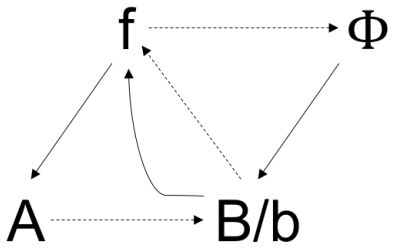

Figure 2.8: An illustration of the causal flows in Rosen's (M,R) system model which is a minimal abstraction of an open, dissipative system that is able to transition to, and maintain, an organised state. The solid lines indicate a material cause and dashed lines indicate an efficient cause. Labelling is expressed in category-theoretic language where: A is the Environment, B is the Repair function, f is the Metabolism function and Φ is the Replication function. Adapted from [90].

at an instant in accord with the model's predictions pertaining to a later instant"[91]. More recently, Karl Friston's energy minimisation model [93] has provided a similar explanation; namely, that a living system aims to maintain its structural and functional integrity through 'active inference' of changes in state of itself and its environment.

Rosen's model is not incompatible with autopoiesis and indeed Francisco Varela suggested the term "intentionality" [44] to convey a similar notion. The effect of intentionality has been investigated using an artificial life simulation [94] with the result that an autopoietic system that embodies even the most basic form of anticipation improves its viability. In this work intentionality was manifested as self-repair of the membrane. Equivalently, the organisation of an autopoietic system is the internal predictive model encoded in the relations between its components that represent knowledge of how to self-produce; the ability to change state based on that model is structurally determined. An exploration of the properties of cellular self-organisation [95] reinforced the criticality of the notion of "closure to efficient causation" in (M,R)-systems to the viability of an organism and that this is synonymous to the concept of "organisational closure" in the theory of autopoiesis.

In general the (M,R)-system and autopoietic theories abstract out the specifics of components and instead emphasise a circular causation as the embodiment of a living system. The intersection of autopoiesis and (M,R)-systems theory has been investigated [92] with the conclusion that autopoietic systems are a subset of (M,R)-systems. If that should prove to be the case, then an autopoietic system must inherit some of the characteristics of a (M,R)-system such as encoding all of the information required for self-production and self-maintenance. And yet, to the best knowledge of this author, there have been no investigations into the information content of an autopoietic system. This unexplored

aspect of autopoietic systems is directly investigated in this project and, as presented in Chapter 4 and discussed in more detail in Chapter 10, I discovered that the ability for a self-producing system to transition to different structural states can be quantified by the Shannon entropy of its current structure.

Whilst (M,R)-systems theory and autopoietic theory share a number of important concepts, the former is based on category theory which is a rather specialist branch of mathematics. This is not without merit for a receptive audience - and, indeed, work has been published on distinguishing between the two theories from a category theoretic perspective [96] - however it was decided early on in this project that the technical nature of category theory risked making the model, and therefore the findings, too inaccessible to a wider non-mathematical audience. Hence, whilst (M,R)-systems would share a common conceptual home with autopoiesis, it would not be central to this project.

Kauffman's collective autocatalysis theory

The description of Kauffman's collective autocatalysis in this section first appeared in a previous report [97] by this author and is reproduced here.

Another closely related model to autopoiesis is autocatalysis [40] or, more precisely, collective autocatalysis [33]. Autocatalysis is a chemical dissipative system [98] that self-reproduces - it consists of a set of chemicals that through their reactions reproduce the chemicals in the set. Under conditions of dissipation and random decay, autocatalytic sets have the potential to reconstruct their own lost components and if the energy input exceeds the energy output then the autocatalytic set grows in volume. If this autocatalytic set is within some form of cellular enclosure then osmotic pressure can cause the container to split (aka. cell fission). Stuart Kauffman [40] proposed and Doyne Farmer et al [99] developed in detail a computational model of polymers that were created through the reaction of smaller and simpler molecules and from which, over time and with a sufficiently diverse population of polymer species, an autocatalytic set formed. The idea is that polymers will emerge from the catalysed reactions of simpler molecules no matter how improbable those initial reactions may be. This assumption built on the results of experimental work by Cavadore [100] and Fox & Dose [101] that showed that small molecules (such as peptides) can catalyse the reactions of other peptides. Kauffman's hypothesis was simple: self-reproduction is a "natural collective expression of polymer chemistry" [40] and the underlying physical mechanism that enables such behaviour is autocatalysis. To achieve catalytic closure in a set of catalytic polymers, Kauffman suggests four steps:

1. All possible polymers up to a critical length M should be available to participate in a

reaction (either as a substrate or as an enzyme)

2. All possible combinations of legitimate reactions that can occur in this set and by which these polymers can be formed from one another should be considered

3. The capacities of polymers to catalyse reactions should be clearly defined i.e. all polymers have the capacity to catalyse a reaction (whilst there is a very small probability that a reaction can occur between two molecules in the absence of a catalyst, these are not included in Kauffman's model)

4. The probability that a set of polymers contains a subset which is reflexively autocatalytic rises to 1 as a critical threshold is reached

In a system of just two molecules representing an initial food set there were $\approx 2^{M+1}$ numbers of polymers that could be produced from the cumulative effect of increasingly complex molecules reacting and producing new molecules. Therefore, as M increased, the number of polymer species increased exponentially. The molecules that participated in the chemical reaction - the catalyst and the substrates - were chosen at random. As the process iterates the proportion of new molecules in the population grows and were more likely to be randomly selected to be a catalyst in a future reaction. In this way, a network of reactions grew over time with simple molecules reacting to create new molecules, which themselves catalyse other reactions possibly those that create their own substrates. If a subset of this reaction network consists of molecules that catalyse and produce each other, an autocatalytic set is deemed to have formed. The conditions for a Kauffman autocatalytic set to form are: (i) in which every reaction in R is catalysed by at least one molecule involved in any of the reactions in R; and (ii) if every reactant in R can be constructed from an initial food set F by successive applications of reactions from R. If both of these conditions are met then it is defined as a reflexively autocatalytic and F-generated (RAF) set [41]. A formal method for detecting and confirming such sets has been described in detail [102]. The emergence of an RAF set is the key mechanism by which more complex chemistry can arise and sustain itself from simple, random precursors. This is the cornerstone of Kauffman's theory.

There is a critical relationship between the probability P of a catalysed reaction occurring and the critical length of polymer M required to form an autocatalytic set. The critical length M is the threshold at which there is a sufficient diversity and number of polymer species 2^{M+1} available to participate in reactions a subset of which form an autocatalytic set. The more improbable a reaction the greater the diversity and the longer

the period of time required for a reaction network to begin to develop. The ratio of reactions to polymers is given by:

$$\sum_{i=1}^{M} \frac{M-i}{2^i} \approx M-2 \tag{2.1}$$

The left hand side of Equation 2.1 is the total number of possible reactions of all polymers at a given length (i) up to the maximum length M, divided by the number of all possible polymer species of length i - which is approximately the same as the maximum length of polymer (M) less the number of different types of monomer constituting those polymers (in this case, the polymers have a binary alphabet hence there are two types of monomer).

The implication of Equation 2.1 is that as M increases the number of polymer species increases. However, the number of reactions occurring increases faster than the number of new polymer species being created. Indeed the ratio of reactions to polymers increases linearly with M. This leads to more legitimate reactions in the system than there are polymers and this imbalance, 'reflects the simple combinatorics of polymer strings made up of two monomer units' [103]. The connectivity between polymers is therefore a key consideration in autocatalysis. Phase transitions in random graphs [104] can provide a succinct explanation of how the connectivity of a network reaches a critical point whereby all vertices are connected to at least one other vertex, thus forming a complete path through the network. Kauffman refers to this connected graph as "one gigantic component" and this characteristic of random graphs is another cornerstone in the theory of autocatalytic sets of proteins.

Kauffman ran a number of simulations to evaluate the model, and a reflexively autocatalytic set successfully formed as a subset within a larger reaction graph. The conclusion of his work was that "... any sufficiently complex set of catalytic polymers can be expected to be collectively autocatalytic" and, as such, "... life may be more probable than we have supposed" [103].

A more recent development of the Kauffman model is Segre et al's Graded Autocatalysis Replication Domain (GARD) model [105] of the primordial chemical selection of mutually catalytic sets (where mutual catalysis is equivalent to network replication as per Eigen & Schuster hypercycles [43]). The model describes how "catalytic closure can sustain self-replication up to a critical dilution rate [which is] related to the extent of mutual catalysis involved" [105]. GARD simulations offer a rigorous kinetic analysis with which to model the behaviour of ensembles of molecules and the spontaneous formation and maintenance of autocatalytic sets. As popular as the GARD model has become it is not

without its limitations. It is claimed that self- sustaining autocatalytic networks - as regularly generated by GARD simulations - do not evolve and, as such, constrain the prospect of metabolism as one of the main mechanisms of the origin of life [106]. A counter-argument [107] is that the GARD model does allow for, and demonstrate, how "evolution-like" behaviour can emerge in molecular systems, on the condition that excess mutual catalysis (network replication) exceeds self-catalysis (self-replication) in the system. The evolvability of autocatalytic sets in the GARD model and the emergence of peripheries of molecules that were maintained by an autocatalytic core but that were not part of the core itself have also been demonstrated [108]. These peripheries act as a form of phenotype and the rate at which they replicate is a measure of fitness compared to other peripheries and other autocatalytic cores thus demonstrating a degree of natural selection (and therefore evolution).

The relationship between autocatalysis and autopoiesis has been investigated [33] and this acknowledged that their formation and organisation are by similar processes with the critical distinction being that an autopoietic systems autocatalytic process generates a spatial boundary. Now, not withstanding the contested nature of spatial boundaries in autopoietic theory, the distinction can be considered more generally as implying that autocatalytic systems are not autopoietic and yet autopoietic systems may consist of one or more autocatalytic cycles. A more fundamental difference - as argued in [109] - is that Kauffman's autocatalytic model of a living system is dependent on a large set of entities (polymers) numbered in the thousands. Kauffman deems this an absolute necessity to achieve the statistical properties required for autocatalytic closure to occur. This requirement is opposite to the model of a living system as devised by Maturana & Varela which implies that a much smaller system should be sufficient for a minimal autopoietic system. However, Kauffman's model is addressing impoverished and under-developed initial conditions i.e. the complete absence of highly efficient catalysts. For example, if any polymer in the system has a probability of 10^{-9} of catalysing a reaction then the "probability of catalytic closure occurring is very low unless there are at least 3×10^8 different kinds of molecules" [109] that are all available to interact with each other at any time. Clearly, more efficient catalysts would reduce the size and diversity of the population required to achieve catalytic closure. It may be the case that autocatalysis acts as the springboard from which more efficient forms of organisation can emerge and that these more optimal configurations are minimal, self-producing and self-maintaining systems that have the sufficient functionality and efficiency of operation to achieve not just catalytic closure but also efficient causation closure (i.e. as required by both autopoiesis and (M,R)-systems). These more efficient forms of organisation then provide the platform for the

emergence of more sophisticated living systems. Autocatalytic cycles formed spontaneously in all of my simulations of a population of interacting automata and, in the context of autopoiesis, I propose that such networks - with properties of dynamically stable, strongly connected components - are a recurring feature of all systems that are developing towards an autopoietic state.

2.2.3 Cognition

Cognition[3] is a process that is, "... an *effective action*, an action that will enable a living being to continue its existence in a definitive environment" (page 29 of [32]). In simpler terms cognition is the process of bringing together the mutual interactions between an autopoietic system and its environment and the subsequent changes to both that occur as a result. More specifically, autopoietic systems are deemed to be structurally coupled to their immediate environment and, as such, undergo dynamic changes due to perturbations from the surrounding medium. "Successful autopoiesis" [88] leads to the selection of a structure which is the most suited to the environment. An autopoietic system is realised by a particular structure and, as the system is structurally determined, this defines the future changes that may be possible. My own research confirms this and, specifically, quantifies the structural states that a given autopoietic system can transform itself to. John Mingers suggests that we think of structural coupling as: "... changes may preserve the structure as it is or they may radically alter it (think of an acorn developing into an oak [tree]) so the structure is said to be plastic. This plastic structure exists within an environment which perturbs it and triggers changes. The environment does not determine the changes but it can be said to select the state from among those made possible at any instant by the system's structure" (p. 168 of [88]).

Two types of interactions between an autopoietic system and its environment have been suggested by Bourgine & Stewart: "*type A* interactions that lead to changes in the internal state of the system, and *type B* interactions that lead to changes in the environment or that modify the relation of the system to the environment" [13]. Distinguishing the interactions in this manner allowed Bourgine & Stewart to propose a more precise definition of cognition: "A system is cognitive if and only if type A interactions serve to trigger type B interactions in a specific way, so as to satisfy a viability constraint" [13].

Type A interactions are referred to as "sensations" and type B interactions as "actions". Type A interactions are mediated by specialised "sensory organs" in the boundary of

[3]According to an interview with Varela (as presented in [8]) he admitted that this was an unfortunate choice of word given the anthropomorphic meaning usually attributed to it.

the system and type B interactions are mediated by specialised "effector organs" also situated in the boundary [13]. As such, they are defining the boundary as the systems interface between the internal organisation (which is maintained via. autopoiesis) and the environment. Hence, "... the sensory input must not only be used to guide the actions in an intelligent way but that, conversely, the actions of an organism also have consequences for its subsequent sensory inputs" (p. 339 of [13]). Whilst I am uncomfortable with the use of the word intelligent here (I prefer to use the word logical) the meaning is quite clear: sensory inputs have a causal effect on the internal structure of the autopoietic structure which, given that the system is structure-determined, will lead to a subsequent change in the sensory inputs in the systems interface.

Bitbol & Luisi [12] suggest that there are two meanings for cognition: (i) the metabolism of a living unit is the most direct form of cognition given the implied continual exchange with the environment both of which form and are formed by each other which they refer to as "a simultaneous coming to being for the organism and for the environment" [12], and (ii) the adaptation of the system to novelty (the authors refer to "new foreign molecules" however I prefer the more general notion of new entities) leading to a change in the metabolic pattern i.e. the underlying networks of production that are continually producing the critical components required to re-generate the autopoietic system. These two forms of cognition are equivalent to Piaget's [110] assimilation and accommodation with the latter arguably more pertinent to the concepts described here.

Piaget's work is grounded in cognitive development from the field of psychology and the meaning of his two terms are best conveyed with the following example [110]: "A child seeing a zebra for the first time and calling it a horse. The child assimilates this information into her schema for a horse. When the child accommodates information, she takes into consideration the different properties of a zebra compared to a horse, perhaps calling a zebra a horse with stripes. When she eventually learns the name of zebra, she has accommodated this information".

Hence, assimilation is the process of making sense of new information/entities by reference to the information/entities that are already present in the system and to attempt to fit the new entity into that model/schema/representation whereas accommodation requires the revision and change to the existing model/schema/representations so that the new information/entity can be incorporated. So, in the context of autopoiesis and Bitbol & Luisi's two forms of cognition assimilation is equivalent to the uptake and exchange of metabolites in the metabolic network, and accommodation is biological adaptation where the system's metabolic network is changed in a way that endures.

Bringing this together autopoiesis (self-production) and cognition (adaptation) are

the two critical processes that generate and maintain a living system. Yet, which of these fundamental processes is the progenitor of an autopoietic system? Is there any primacy between these two processes: i.e. does a basic form of autopoiesis need to form before the system is able to perform any kind of cognition? What is the nature of their co-creation and co-dependency? Is one process sufficient for a system to be autopoietic? Bitbol & Luisi examined this and concluded that "autopoiesis alone is only a necessary, but not sufficient, condition for life" [12]. In other words, some form of cognition is required for life. The claim that autopoietic systems require a basic form of cognition is worth exploring further as it may yield insight into the critical stages and properties of proto-autopoietic systems that enables them to become fully autopoietic. I explicitly examine the assimilation/accommodation behaviour of a proto-autopoietic system with the development of the information niche model that emulates an influx of new entities (molecules) from the environment (see Chapter 7). To examine cognition in the type A/type B forms proposed by Bourgine & Stewart I developed the computation niche model (see Section 3 and 8) which explicitly models a systems interface (boundary) as an information processing component that receives and transduces information from the environment (type A) that leads to internal changes in the structure of the system. Such changes lead to changes in the systems interface and also changes in the information emitted by the system into the environment. The emissions have the effect of modulating environmental information (type B interaction) which, in turn, is received by the systems interface thus completing an operationally closed cycle. The conclusions I draw from these studies is that a self-producing system that consists of hierarchical, dynamically stable and strongly connected networks are very robust to environmental perturbations. I also show that the underlying interaction network that drives the behaviour of the internal population adapts readily to new types of entities although this does not necessarily lead to a change in the structure of the system as a whole (i.e. the system is assimilating but not accommodating).

Evolution is the "change in heritable characteristics of biological populations over successive generations" [111] or, more generally, the gradual development of something. Darwinian evolution [112] states that organisms develop through natural selection of minor variations that occur over time and that may increase the organism's ability to compete and reproduce. As such, it is a theory of how biological evolution occurs. Humberto Maturana has proposed [7] that autopoietic systems evolve - in the general (non-Darwinian) sense of the word - by the continual interactions between environment and the system where the system regenerates and optimises its organisational states for maintaining its identity. The plasticity of the system - facilitated by the cognitive process of accommodation - in response to changes in the environment over time leads to natural drift. Natural

drift is a dynamic process that affects the structure of an autopoietic system which over cumulative adaptations forms a historical product [29]. Bitbol & Luisi [12] declare that for an autopoietic system to evolve requires that as a minimum Piaget's accommodation is possible.

2.2.4 Limitations of Autopoietic Theory

The three prevalent issues in the field of autopoiesis are:

The conceptual gap between autopoiesis and Darwinian evolution.

Autopoietic theory has been studied extensively [12],[13],[14],[2],[15],[16] (also see Figure 2.2) and yet it has not had a substantial impact within its field of origin which was biology. This has been investigated [27],[6] with the conclusion that (a) the lack of any emphasis on DNA, in the theory of autopoiesis, at a time (in the early 1970's) when DNA/RNA dominated discourse of the behaviour of biological systems and the prevalent scientific worldview was almost entirely reductionist, and (b) the lack of any convincing explanation of evolution and, specifically, to Darwinian evolution. Addressing the former has been largely rectified [6] whilst several attempts to address the latter [7],[28],[29], [30] have remained inconclusive. Advocates of autopoietic theory can rightly demand greater clarification from Darwinism especially about the lack of serious questioning of the assumptions of natural selection as the primary mechanism (a largely philosophical issue given the phenomenological basis of Darwin's theory) whilst critics of autopoiesis may demand more evidence for evolution of such systems in the absence of genetic machinery [30]. Is there a possible contribution that the theory of autopoiesis can make to addressing the remaining theoretical issues of Darwinian evolution? As is discussed in Chapter 10 I believe that my research takes steps towards showing a unification of these two theories through the fundamental mechanism of competition. Clearly natural selection as a core mechanism of Darwinian evolution has a competitive element. From my own research I have observed that the behaviour of proto-autopoietic systems can be explained by competition between interacting entities, networks and populations. Such multi-level selection - survival of the most competitive - was present where a selective pressure existed (e.g. a finite population size). Competition between automata - and the networks that they form - in my simulation model led to the growth and decay (and eventually extinction) of some automaton types which led to the population structure reaching a steady-state within a given environment. The populations of automata transform via. a selection process with the emergent structure representing the best "fit" to the environment. This is why I refer to these steady-state structures as niches. The idea that a fundamental mechanism of autopoietic operation is a competitive

process, that extends into and persists throughout the Darwinian evolution of biological systems, could be a new insight arising from my research.

Autopoietic systems are uncomputable.

If we accept that an autopoietic system is a sub-class of (M,R)-systems then by association they are also closed to efficient causation and as such are non-computable [92]. This is a feature of (M,R)-systems that was demonstrated by Robert Rosen but which remains a controversial and contested topic [109]. In essence, this non-computability claims that autopoietic systems cannot be modelled or simulated computationally [92]: “The non-computability of autopoietic systems, as advanced here, apparently collides with the simulation results involving tessellation automata. But new versions of this simulation show that the original report of computational autopoiesis was flawed, as it used a non-documented feature involving chain-based bond inhibition. Thus the closure exhibited by tessellation automata is not a consequence of the "network" of simulated processes, but rather an artefact of coding procedures”. However, this claim has been strongly refuted by McMullin who in collaboration with Varela identified and corrected the original model. In his own words: “... the overall thesis of Letelier et al. of the "non-computability" of autopoietic systems - should be taken as refuted, rather than corroborated, by [our] results” [113]. Hence, the non-computability of autopoiesis is a contested issue and the acceptance and weight given to any research findings generated from my simulation results will be interpreted with respect to the reader’s own views on this matter.

The criteria for a physical boundary remains contested and unresolved.

As has already been discussed in this chapter the requirement for a self-producing system to have a physical boundary for it to be deemed to be autopoietic is a contested issue. There appears to be a trend in the field away from such a prescriptive requirement (e.g. Virgo et al’s work on extended autopoiesis [16], Luhmann’s work on social autopoiesis [18]) and towards acceptance of non-physical boundaries. This has important implications for how the findings of my own research are interpreted and the basis of any claims that I make.

2.3 Computational Models of Autopoiesis

Since the inception of the theory of autopoiesis, there have been a number of computer simulations of autopoietic-like behaviour. The original computational model of autopoiesis, Varela et al’s Substrate-Catalyst-Link model [9] was the progenitor of all other models and this is introduced shortly. Fontana’s Algorithmic Chemistry [46] and Crutchfield &

Gornerup's Finitary Process Soup [36] are the models that most closely align with my research aims and those, too, are discussed in this section.

The field of computational autopoiesis is, of course, much richer than these three models and here I wish to acknowledge such work: Breyer et al's self-assembling structures [114], Ono & Ikegami's artificial chemistries on a lattice [115], Beer's exploration of autopoiesis in 'the Game of Life' [116], Wiedermann's autopoietic automata [117], De Loor et al's simulations of abstract autopoietic machines [118], Wang et al's lattice model of emergence and maintenance of an autopoietic system [119], and more recently, Matsufuji & Narikiyo's simulations of the evolution of autopoietic cells [120]. Whilst they are all of merit in their own right I do not discuss them further.

2.3.1 Substrate-Catalyst-Link (SCL) model

The description of the Substrate-Catalyst-Link model first appeared in a previous report [121] by this author and is reproduced in part here.

Varela et al. [9] developed the first computation model of an autopoietic system which successfully demonstrated the formation and maintenance of a boundary around an internal reaction that was producing the product that formed the membrane. The reaction schema for their ideal chemistry is shown in Figure 2.9.

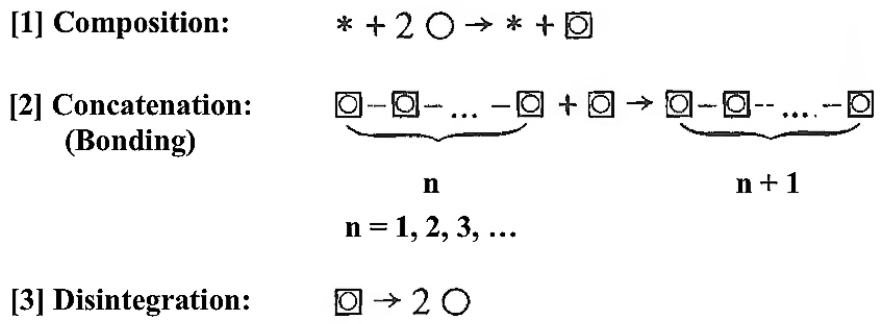

Figure 2.9: The schema for the ideal chemistry of Varela et al's SCL model of autopoiesis. Taken from [9].

Figure 2.9 outlines the three reactions that constitute the artificial chemistry of the Substrate-Link model:

Reaction 1: the composition of two substrate molecules (circle) into a link molecule (circle in a square) catalysed by the catalyst molecule (star). The link product feeds Reaction 2.

Reaction 2: the bonding of a link molecule onto an existing link chain that will form the membrane boundary.

Reaction 3: the disintegration of a link molecule to two substrate molecules that potentially leaves a hole in the link chain that constitutes the membrane.

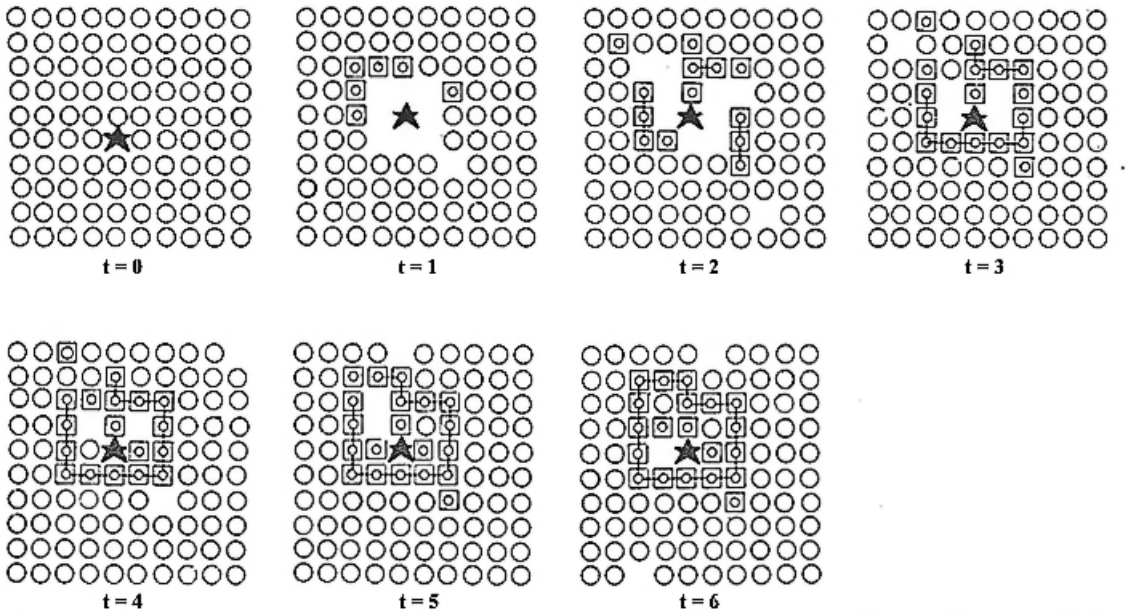

Figure 2.10: Over six successive time-steps ($t = 0$ to 6), a catalyst (the star) transformed substrate molecules (the circle) into membrane molecules (circle in a square) which bonded to compartmentalise the catalyst and substrate molecules to produce more membrane molecules. Taken from [9].

As shown in Figure 2.10 a tessellated grid was initialised with all locations occupied by substrate molecules and a single catalyst molecule at $t = 0$. In successive time-steps $t = 1$ to 6 the composition (Reaction 1) and condensation (Reaction 2) reactions occurred with formation of the link molecules that subsequently bond to other link molecules. At the end of this snapshot of the simulation ($t = 6$) the catalyst molecule has become enclosed by link molecules. Varela's model assumed that link molecules were semi-permeable and that allowed substrate molecules to diffuse through unhindered. Conversely, the catalyst molecule was unable to migrate through link molecules.

In later time steps ($t = 44$ to 47) the disintegration of a link molecule (Reaction 3) left a hole in the link-chain. This was subsequently repaired by the production of another link molecule and its subsequently bonding to the link-chain thus repairing the hole in the membrane (see Figure 2.11). With the SCL model, Varela et al. successfully demonstrated the basic concepts of autopoiesis.

Attempts to repeat Varela's simulation were not routinely successful [11] and a subsequent investigation led to the identification of "chain bond inhibition" as a critical rule in

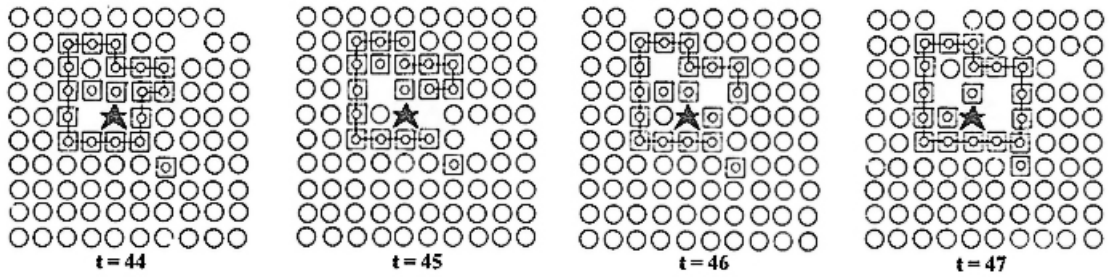

Figure 2.11: In later time-steps (t = 44 to 47) the Varela simulation demonstrated the repair of the membrane. Taken from [9].

the simulation. This rule only allows link-link formation at the terminal ends of the link molecules or the terminal ends of link-link chains; a corrected version of the model was implemented and the simulation results confirmed Varela's earlier results [45].

A 3-D tessellation automaton was implemented to demonstrate a more complete and physically realistic demonstration of autopoiesis [13]. This minimal model of autopoiesis was based on a spherical membrane enclosing an internal volume. The semi-permeable membrane was a two-dimensional sheet that decayed at a given rate to leave holes. Internal reactions generated the membrane product which diffused from the interior to the outer boundary where they filled holes in the membrane. Conceptually their model was similar to the original model with the exception that it was implemented as a three dimensional entity. This more realistic model equipped Bourgine & Stewart with the means to critically examine the definition of autopoiesis and cognition, as they observed from their simulations, and which led them to suggest the following clarifications to autopoietic theory: "(i) An autopoietic system is a network of processes that produces the components that reproduce the network and that also regulates the boundary conditions necessary for its ongoing existence as a network, and (ii) A system is cognitive if and only if sensory inputs serve to trigger actions in a specific way, so as to satisfy a viability constraint" [13].

They conclude that, "... a system can be autopoietic without being cognitive, and cognitive without being autopoietic" [13]. They theorise that: (i) an autopoietic system is a random dynamical system that is defined only within its organised autopoietic domain (that is, it is not dependent on any external source for constructing itself); and (ii) a system that is both autopoietic and cognitive is a living system. The first of these points does not explicitly denounce "extended autopoiesis" [16] but rather simply states the possibility that an autopoietic system can form in the absence of any dependency on external processes. Bourgine & Stewart conclude with the observation that more work is required to explore the increasing complexity of the simulation of autopoietic systems such that: "a [network]

of reactions so much richer... that the probability of it having emerged from an environment of the same level of complexity is close to unity" [13].

This is consistent with Kauffman's hypothesis [103] that once a chemical reaction network surpassed a certain threshold of complexity then autocatalysis was likely to occur. However, whilst autocatalysis - more specifically, collective autocatalysis [33] - is a likely requirement for an autopoietic system it does not necessarily satisfy the criteria for an autopoietic system as has already been discussed.

These models - the original Varela computational model and the Bourgine & Stewart work - suffer from two serious limitations in addressing the research aims of this project: firstly, they are extremely limited in their ability to consider other factors such as the effect of environmental perturbations, reproduction and heredity and interactions with other autopoietic systems; and secondly, and most critically, they are totally reliant on assuming the presence of an ideal qualitative chemistry which by design overcomes the need for their model to demonstrate how a "network of reactions" would form in the first place. To explore autopoiesis and to further demonstrate its applicability to systems chemistry approaches to protolife it is therefore important to look to computational models that demonstrate how autopoiesis and cognition processes may form in the absence of any pre-determined selective chemistry. Such models will need to allow for a system to increase the number of, and diversity of, its components and processes from initially simple populations. These populations should also have the potential to undertake preferential interactions, to self-organise and to generate self-producing behaviour. Such models exist and are known as artificial chemistries [90].

2.3.2 Algorithmic Chemistry

The description of the Algorithmic Chemistry model in this section first appeared in a previous report [121] by this author and is reproduced in part here.

Algorithmic chemistry (AlChemy) is an artificial chemistry whose molecules are represented as mathematical functions [4] that can interact with other mathematical functions [46]. The interaction between these functions generate a new function, by the mathematical operation of functional composition, whereby the new function inherits the domain (the input) of the first parent function and the range (the output) of the second parent function. Not all interactions yield a valid function and these are prohibited and essentially

[4] A mathematical function is simply a mapping from one domain to another and represents a transformation e.g. the multiplication (×) function takes as input the numbers '2' and '8' and outputs the number '16'.

ignored. Algorithmic chemistry is based on the λ calculus which is a minimal language of computation.

More formally, functions are represented as λ-expressions. Each unique λ-expression has the possibility of operating on other λ-expressions and, by doing so, transforms that expression into a new λ-expression. However, unlike a normal chemical reaction, the reactants (the λ-expression that transformed the other λ-expression) do not get consumed in the process and continue to exist alongside their new child operator. Instead, as one new operator is created another one is randomly selected and removed from the simulation. As such, the overall population size is kept constant and creates a form of selective pressure between operators to replicate and/or to form mutually replicative networks of interactions with other operators.

Each function is a λ-expression which simply denotes the syntax and language used to describe a function. In simple terms: a function receives a variable, processes that variable in some manner determined by the internal structure of the function, and outputs a variable. Each λ-expression is a mini-algorithm that describes how to process the variable received by the function. As these molecules collide the collision can be reactive (a product molecule is produced) or elastic (no product molecule is produced). If two molecules react then the product molecule is the result of functional composition i.e. the input to one function f is the output from the other function g written as $f(g)$.

The following algorithm that describes how these molecules react [46]:

1. Select two functions from the population
2. Test whether their collision is reactive or elastic
3. If reactive then add the product molecule into the population; remove another - randomly selected molecule - from the population to maintain a constant population size
4. If elastic then no product molecule is produced
5. Repeat

This collection of functions - which are essentially interacting strings of characters in the language of λ calculus - that collide, react and create - is known as a "Turing Gas" which Fontana simulated under various scenarios [46].

Turing Gas without Perturbations. Fontana simulated an initial population of 1,000 randomly generated and unique functions evolved over 10^5 iterations involving 100,000

reactions that led to the creation of 18 new functions that were not present initially. This led to a quasi-stationary state of the system that self-organised from random initial conditions. Fontana offered this as evidence that the AlChemy model could generate innovation. The relationship between the 18 functions that remained at the end of the simulation (all others were diluted out of the population) were described as an interaction graph that was autocatalytic, closed and that did not consist of any parasitic sets.

Turing Gas without Copiers. The second set of simulations set the boundary condition that no copying functions were allowed. Some functions are identity functions - that is, when they react with another function the product is identical to the non-identity function - and they are universal copiers. Other copiers are "partial copiers" meaning that they create a copy of themselves or the function they are reacting with but they only do this with a subset of functions in the population. In running simulations of this type Fontana identified three absorbing states for the population:

- heterogeneous mixture of elastic colliders (dead system)
- a single self-reproducing function
- a self-reproducing set in which every function is a seeding set (this absorbing state was described as a quasi steady-state)

This experiment also revealed that:

- innovation decays fast
- the trend towards closure of the population is based on the appearance of identity functions and partial copiers
- functions not linked to transformation pathways are eventually displaced by dilution (removed from the population)
- nesting of autocatalytic components is a frequently observed pattern

Fontana summarised his findings as [46]:

- the only way for a function to survive is to become part of some transformation pathway
- a transformation pathway survives by becoming closed (self-maintaining)

- stability of self-reproducing sets (of functions) is strongly influenced by the number and size of the initial seeding sets (functions created under initial conditions)

The AlChemy model demonstrated the formation of three hierarchical levels of organisation:

Level 0. The operators (objects) in the system only perform one type of operation - an identity operation and thus self-replication. Within a Level 0 organisation it is possible that a hypercycle [43] emerges whereby operators mutually copy one another.

Level 1. By prohibiting the identity function a different organisation emerges. In the words of Fontana: "... at the syntactical level there exist common regularities that characterize the structures of all operators maintained in the system. These regularities define a grammar, i.e. lawful arrangements of identifiable substructures.... furthermore, when new operators are created from interactions within the system, their structure conforms with the grammar.... the subspace specified by the grammar is invariant as interactions proceed; closure has been attained" [46]. Fontana's invariant subspace bears similarities to the invariant frequency distribution of a single state finitary process soup (see Section 2.3.3). These laws specify the relationships between objects whose structure conforms with the specified grammar. Overall a system that attains such properties is behaving as a single object and this invariant entity is called an "organization" [46]. Indeed a Level 1 organisation is conceptually equivalent to a Crutchfield & Gornerup 'meta machine' in the finitary process soup (see Section 2.3.3).

Level 2. Self-maintaining organisations (Level 1) that are combined in some manner have the potential to create Level 2 organisations. Level 2 organisations are characterised as two or more Level 1 organisations that co-exist with cross-interactions producing new operators that do not belong to either organisation. These interstitial operators act *as a glue* (according to Fontana) that links, or integrates, the Level 1 organisations in a higher order unit. This is an interesting result as it is a demonstration of two autopoietic systems becoming structurally coupled which could be indicative of a pathway to multicellularity.

Although not mentioned by Fontana, there appears to be an association between Level 0 and Level 1 organisations with the autopoietic process, and Level 2 with the cognition process. Furthermore, there is a close similarity between Fontana's operators and "organizations" with Crutchfield's ϵ-machines and meta machines (to be discussed shortly). Fontana's model succeeds in demonstrating an increase in the complexity of initially simple

and unconnected unity's into hierarchical organisations from an initial achemical state and - through the mutual transformations that emerge - begins to exhibit chemical behaviour with the formation of sustained networks of interactions (i.e. autocatalysis).

However, the model has a number of limitations: (i) as networks become more complex the ability to detect and analyse the existence of separate organisations in the Turing Gas becomes problematic; (ii) there does not appear to be a natural extension of the model to a spatial dimension, and (iii) the model - based on λ-expressions does not allow for a straightforward estimation of the information content of the "Turing Gas" or any organisations present within it. In a sense, the AlChemy is too minimal (or abstract) to allow a more detailed pursuit of the research goals of this project.

Such limitations - particularly the difficulty with which to identify organisations in an increasingly complex Turing Gas - were partly addressed by Peter Dittrich and Pietro Speroni di Fenizio with their theory of chemical organisation [77]. Their approach consisted of two parts: (i) they defined a chemical organisation as a closed and self-maintaining set of components which explicitly linked an interaction network with the set of possible organisations that could be generated by those interactions; and (ii) mapped the set of organisations to a state space. This two step process was represented as a differential equation that describes the chemical dynamics of the network and, as such, every stationary state that could be found was an instance of an organisation. This was an elegant solution to the first of the limitations of the AlChemy model as described above. However, it did not address the remaining issues and for that we have to turn to Crutchfield & Gornerup's Finitary Process Soup model.

2.3.3 Finitary Process Soup

The Finitary Process Soup (FPS) model - developed by James Crutchfield and Olaf Gornerup [36] - was adopted as the underlying model for my project that I subsequently developed into the information niche and computation niche models (see Chapter 3). In this section the FPS is introduced in general terms followed by a brief discussion on its limitations. A more detailed explanation of the model is described in Chapter 3.

The FPS is an abstract approach to studying prebiotic mechanisms that, in a similar way to the AlChemy model, makes no assumptions about a pre-existing chemistry. Crutchfield & Gornerup define a population of entities that can interact. Each entity represents a function, specifically, an information processing function i.e. they process binary information (bits). Functions receive binary information, process that information in some way, and then emit binary information and they can do so in increasingly complex

and well-defined ways. Hence, as was the case with the AlChemy model, functions can interact with each other and their product is a new function via. the process of functional composition. However, where Fontana chose λ-expressions to represent these functions Crutchfield & Gornerup chose to represent functions as a special class of finite state transducer called ϵ-machines. ϵ-machines are minimal representations of unique stochastic processes and the manner in which they are defined, and the basis for their interaction with other ϵ-machines, follow explicit rules for evaluating functional compositions. Only valid ϵ-machines were allowed in the FPS model.

As ϵ-machines interact with other ϵ-machines over extended periods of time (10^6 iterations is normal) the overall structure of the population reaches a steady-state where the frequencies of each object become invariant. These invariant distributions are called "meta machines" and are deemed to be analogous to an autocatalytic set. Each ϵ-machine's internal structure can be quantified precisely by estimating its structural complexity [37]. Furthermore, the structure of the population can also be measured by estimating the interaction network complexity [36]. The ability to quantitatively measure the structure of individual entities and their collective organisation directly addresses the first and third limitations of the AlChemy model.

Simulations of the FPS model by Crutchfield & Gornerup [36] revealed that an initially uniform population of ϵ-machines self-organise to a steady-state distribution that persists over time - a meta machine. This meta machine represented a “global complexity [that was] due to the emergence of higher level structures and this in turn is facilitated by the discovery and maintenance of relatively non-complex, but general objects” [36]. "General objects" refers to the most simple ϵ-machines (i.e. one-state finite state automata) and 'higher level structures' is referring to the underlying network of production that emerged as the population evolved. Crutchfield & Gornerup's intimation that such meta machines are autopoietic is questionable as their work does not demonstrate any kind of perturbation that may disrupt the identity of the meta machine, and therefore test the presence of a cognitive (or adaptive) process. The persistence of automata in a steady-state configuration in their model is indicative of, at least, the presence of self-production, and therefore their work demonstrates the emergence of some but not all of the basic processes of an autopoietic system.

The FPS model has a number of distinct advantages over the AlChemy and the Substrate-Link model:

1. The structure of ϵ-machines can be quantified using structural complexity which is derived from algorithmic information theory [122]. This presents an objective

measurement for the complexity of individuals within a population, and how the complexity of the population changes over time. Such a measurement is not feasible with either the AlChemy or Substrate-Link models.

2. The model is grounded in information theory and computation theory which are two well defined and researched fields.

3. Work by Piantadosi & Crutchfield [123] added a spatial dimension to the FPS model, and their results showed the emergence of spatial patterns that were reminiscent of boundary formation.

However, the FPS model has a number of limitations:

1. The emergence of a steady-state structure that persists through the formation of self-producing networks is a clear example of proto-autopoietic behaviour. However the FPS model does not demonstrate autopoiesis as the process of cognition is not demonstrated (a limitation which is addressed by this project).

2. The role of the environment in the population dynamics is limited to an influx of ϵ-machines. The effect of short-range vs. long-range interactions is therefore excluded. Later unpublished work [123] adds a spatial dimension which partly addresses this issue (see Chapter 3) and yet this model was also too limited in that it did not allow for environmental perturbations. The information niche model addresses all of these issues and is described in Chapter 3 and the results of simulating the model are presented in Chapters 4 - 7.

3. There is no mechanism for examining emissions or outflow from the population into the environment and the effect that this may have on the subsequent feedback from the environment on population dynamics. This is required for examining structural coupling. Addressing this issue required the extension of the FPS model to specifically model a systems interface between the interacting population and the environment. The model that was developed to address this is called the computation niche model and this is described in Chapter 3 and the results of simulating the model are presented in Chapter 8.

4. ϵ-machines are information processing objects and yet their functional behaviour is not examined in any of the models developed by Crutchfield & Gornerup [36] or Piantadosi & Crutchfield [123]. For example, each ϵ-machine represents a unique stochastic process and yet its intrinsic information processing properties are only

used to determine the information processing properties of potential offspring. This omits the interesting possibility of examining the behaviour of the process that it represents. In other words there is a duality to ϵ-machines: (i) they are interacting entities that produce other entities via. functional composition, and (ii) they are information processing objects that receive, process and transmit information. The former is the only aspect of an ϵ-machine that is considered in the FPS model. This is not necessarily an issue but rather a missed opportunity. The computation niche model that I have developed makes full use of the dual nature of an ϵ-machine by modelling interactions between them as per the FPS model but also by modelling their information processing behaviour in an explicitly defined systems interface (a membrane) between an internal interacting population and an environment.

5. Interactions between steady-state populations are not supported by the FPS model. As such, important concepts of autopoiesis such as reproduction and heredity cannot be examined. This is addressed by the information niche model and the results of simulating inter-population exchanges as reported in Chapter 7.

These limitations are specifically addressed in this project with the development of the information niche and computation niche models which are discussed in the next chapter.

2.4 Summary

This chapter has introduced the theory of autopoiesis as a minimal model of a living system that whilst minimal and simple in concept provides a theoretical continuum from the formation of the most basic living system (a protocell) to systems of significant complexity such as human cognition and social systems. A comparison to other models of living systems highlighted the general and universal nature of the theory and therefore its attraction as a framework for understanding the system logic of a basic living system. The state-of-the-art in the field of autopoiesis has been presented and the current limitations in the field discussed.

This chapter also examined computational models of autopoiesis from Varela et al's original algorithm [9] (the Substrate-Catalyst-Link model) and related tessellation models [13] that were reliant on the pre-existence of an ideal and well-defined chemistry to more abstract and bottom up models that emphasised the emergence of organisational forms from undefined and simple beginnings such as Fontana's algorithmic chemistry [46] and Crutchfield & Gornerup's Finitary Process Soup [36].

This chapter concluded with an explanation of the benefits and limitations of the Finitary Process Soup model and this leads naturally into the next chapter where the enhancements and extensions that are made to this model - the information niche model and the computation niche model - are described in detail.

CHAPTER 3

MODELS AND METHODS

3.1 Introduction

This Chapter describes the methodology, models and methods that were adopted, developed and implemented in addressing the Research Aims (as described in Chapter 1). Two computational models are described, the information niche model (see Section 3.3) and the computation niche model (see Section 3.4). Both models were implemented in the MATLAB programming language (see Appendix 12.2). The quantitative methods that were used to analyse and characterise the simulation results were drawn from information theory [124] and network theory [49] and the specific methods used and their application are described in Section 3.5 and 3.6 respectively. A significant number of simulations of both models were run with various simulation set-ups that makes it impractical to discuss them in this chapter. Instead, the introduction to each of the Results chapters (Chapters 4 - 9) explains the specific set-up of the information niche or computation niche model relevant to the results that are presented in that chapter.

The Finitary Process Soup (FPS) model [36] was a model of a population of interacting finite state automata that produced new automata via. those interactions. Simulations of the model revealed that a population would self-organise to a persistent steady-state thus demonstrating a basic process of autopoiesis (i.e. self-production). The rationale for selecting the FPS model as the starting point for the development of my own computational models was explained in Chapter 2 (see Section 2.3.3). The FPS model had the following limitations: (a) no provision for altering environmental conditions during the simulation to

emulate perturbations and therefore no way to examine the robustness of the system nor the degree to which it can maintain its identity, and (b) the inability of the model to support any kind of detailed investigation into the cognition process of an autopoietic system e.g. how an interacting population can adapt to environmental changes or perturbations.

To address these limitations three major developments to the FPS model were made:

1. The ability to instigate environmental perturbations was introduced by allowing abrupt or incremental changes to environmental parameters. This created a 'fitness landscape' through which the population could evolve to different steady-state niches and from which the relative robustness of these self-organising populations could be assessed (see Section 3.3).

2. The transfer of entities between populations was introduced to model and simulate the 'accommodation' form of the cognition process (see Section 3.3.3).

3. The development of an innovative model of a membrane that would act as the system interface between an interacting population and its environment (see Section 3.4). This allowed the nature of the cognition process of an autopoietic system via. its structural coupling with its environment to be modelled and examined.

These additional developments were necessary to generate a sufficient level of data - both in terms of variety and volume - to allow the research aims to be investigated. Developments (1) and (2) were implemented in the information niche model (see Section 3.3) and (3) was implemented in the computation niche model (see Section 3.4). A niche was defined as a state of the population of interacting automata at dynamic equilibrium.

The information niche model was an enhancement to the FPS model[1] [36],[123] that allowed the nature and dynamics of the production processes that generated and maintained a self-producing population to be examined under a wide range of environmental conditions. An information niche was defined as a steady-state population of automata that were generated and maintained through dynamically stable, strongly connected networks of mutually producing automata.

The computation niche model was an extension to the information niche model that explicitly defined a systems interface (a membrane) between an internal population of interacting automata operating under well-mixed conditions and an environment that was generating binary information. The membrane was a network of finite state automata

[1]A description of the FPS model has been subsumed into the description of the information niche model (Section 3.2 and Section 3.3) with the enhancements that were developed during this project identified where appropriate.

(belonging to the ϵ-machine class) that received and emitted information to each other whilst also simultaneously processing information that was received from the environment. The activity of the membrane automata had a direct effect on the interactions that occurred in the internal population and subsequently changes to the composition of population automata. Reciprocally the composition of the internal interacting population dictated the weightings given to the edges of the membrane network which subsequently influenced the flow of information over the network. Furthermore, transmissions from the membrane automata were aggregated into a single emission from the niche into the environment where it modulated environmental information. Examination of the results of simulating this model revealed that the three processes of computation - information transfer, information modification and information storage - were present. This led to a computation niche being defined as a steady-state population of automata that were generated and maintained through the continuous transfer, storage and modification of information that was an intrinsic property of the production and computation processes occurring between the interacting population, the membrane and the environment. Table 3.1 compares the main attributes of each model.

Analysis of the simulation results from both models used methods from information theory and network theory. From information theory, Shannon's information entropy [48] was used to measure the information content of steady-state populations (see Section 3.5.3) and the complexity of the population (see Section 3.5.2) and the structural complexity of individual automata (see Section 3.5.4). From network science, graph theory was used to represent the membrane of the computation niche model (see Section 3.4.2), the interaction relationships between automata in the population (e.g. the interaction network, see Section 3.6.1) and the structure of such a network (see Section 3.6.3) proved useful when analysing the dynamics of the interacting population. These information-theoretic and network-theoretic methods and how they were applied to the information niche and computation niche models are described in Section 3.5 and Section 3.6 respectively.

3.2 Automata

The basic units of interaction in the information niche and computation niche models were finite state automata (simply referred to as automata) [125]. Automata were a special class of finite state transducers (ϵ-machines) that could read a binary alphabet i.e. accept a binary input x, process that information according to the internal structure of the automaton $f(x)$, and emit a binary output y (see Figure 3.1). As these automata belonged to the ϵ-machine class they had to adhere to the following properties [126]: (i) with the

model attribute	**information niche**	**computation niche**
units of production	one-state & two-state automata	one-state & multi-state automata
internal environment	square lattice	well-mixed reactor
selective pressure	random replacement	random replacement
membrane	parameter	automata network
environmental perturbation	rate of influx of new automata (Φ_{in})	environmental information magnitude (Φ_{env})
perturbation effect	global	local
population mobility (diffusion)	variable (zero diffusivity to well-mixed)	fixed (well-mixed)
material influx	random generation of new automata	none
information influx	none	environment information aperture (Φ_{env})
adaptation	accommodation / assimilation of foreign automata	structural coupling via modulation of the environment
reproduction	inter-niche exchange of automata	N/A
novelty	N/A	open-ended production of new automaton types

Table 3.1: A comparison of the attributes of the information niche and computation niche models.

automaton represented as a graph with states as vertices and transitions as edges then it should form a single strongly connected component, (ii) all transitions were deterministic whereby the current state and the next input symbol were sufficient to determine the next state [2], and (iii) the automaton was minimal in that it was the smallest representation of the information processing function that it represents. The information processing function of an ϵ-machine was determined by its number of states and the transitions between those states. There were a total of four possible transitions from each state represented as a pair of input and output symbols (0 | 0,0 | 1,1 | 0 and 1 | 1). The combination of states and transitions was unique to each type of ϵ-machine.

Formally, an automaton (T_i) was the tuple:

[2]This is in the strict sense that the next transition of an ϵ-machine wasn't determined probabilistically and it was entirely acceptable for there to be two transitions leaving the current state triggered by the same input symbol and, in such cases, the transition that was taken was determined with equal probability.

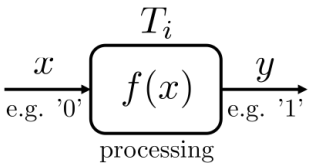

Figure 3.1: An automaton was an information processing function that mapped an input (x) to an output (y) according to its internal structure ($f(x)$).

- Q was the finite set of states of the automaton labelled as $Q = \{A, B, C...\}$. Hence, the length of the set ($|\,Q\,|$) was the number of states that the automaton consisted of.
- A was the finite set called the alphabet of the automaton where $\mathrm{A} = \{0, 1\}$
- δ was the state transition function $Q_i \times \mathrm{A} \rightarrow Q_j$
- S was the symbol set $S = \{x, y\}$ consisting of strings over the alphabet A where x was the input symbol and y was the output symbol of a state transition

The state transition function (δ) could be represented as a $|\,Q\,| \times |\,Q\,|$ table or graphically as shown in Figure 3.2 for a two-state automaton.

(a)

from \ to	A	B
A	0 | 1	1 | 1
B	0 | 0	1 | 0

(b)

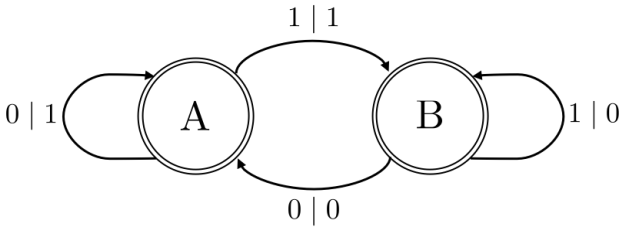

Figure 3.2: (a) The function of a two-state automaton represented as a state transition table indicating the input and output symbol pair ($x \mid y$) for each transition from a state. The input symbol to an automaton dictates the transition that it takes from its current state. For example, on receiving the symbol '1' whilst in state A this automaton would take the transition $A \rightarrow B$ and output the symbol '1'; (b) a graphical representation of the same automaton where the circles indicate the state of the automaton and the directed arrows indicate the from/to relationship of transitions from those states. Each edge is labelled with the input/output ($x \mid y$) pair. Please note: the representation of each automaton state as a double-bordered circle indicates that any state can also be a start state. This is the correct representation of the states for an ϵ-machine class automaton however start and end states of an automaton are not relevant in how they are implemented in the information niche and computation niche models.

Box 3.1 Software representation of automata

Each automata was represented in the simulation program as a list with the states encoded as follows:

$$\text{Q: A,B,C, ... , n} \quad \rightarrow \quad \text{1,2,3, ... , n}$$

, and the transitions encoded as:

$$\begin{array}{l} 0 \mid 0 \quad 1 \\ 0 \mid 1 \quad 2 \\ 1 \mid 0 \quad 3 \\ 1 \mid 1 \quad 4 \end{array}$$

A state transition was therefore represented as δ_{ij} : [start state, symbol pair, destination state] e.g. δ_{AB} : [142] represented the transition $A \rightarrow B$ with the symbol pair 1 | 1. This coding scheme was applied to all automata e.g. the automata shown in Figure 3.2 was represented as the list:

$$\begin{array}{l} \delta_{AA} : [121] \\ \delta_{AB} : [142] \\ \delta_{BA} : [211] \\ \delta_{BB} : [232] \end{array}$$

See Section 12.2 of Chapter 12 for more information on the software implementation of the information niche and computation niche models.

The result of an interaction between two automata (T_a and T_b) was determined by performing the functional composition $T_b \circ T_a = T_c$ whereby the new automaton (T_c) inherited the domain of the first automaton (T_a) and the range of the second automaton (T_b). An interaction was only successful when the range of automaton T_a overlapped with the domain of automaton T_b. Where there was a partial overlap between the range of T_a with the domain of T_b then a partial composition occurred - see the schema in Figure 3.3 and the illustrated example in Figure 3.4. The functional composition was a non-commutative relationship where $T_b \circ T_a \neq T_a \circ T_b$.

There were four possible outcomes from automaton interactions:

- No production - the interaction between two automata was not successful as the range of T_a did not exist in the domain of T_b. Such interactions produced a transitionless automaton (T_0) which was forbidden in the model as in any interaction with other

(a)

$$\begin{matrix} T_a : D_a \rightarrow R_a \\ \\ T_b : D_b \rightarrow R_b \end{matrix} \quad \longmapsto \quad T_c : T_a^{-1}(D_b) \rightarrow T_b(R_a)$$

(b)

Figure 3.3: The composite function from the functional composition of two existing automata: (a) the composite automaton inherits the domain of the T_a automaton and the range of the T_b automaton - the mapping of both the domain of T_a and the range of T_b to the new automaton is partial where the overlap of the range of T_a with the domain of T_b is not total; (b) a pictorial representation of the composition rules indicating that the range of T_a and the domain of T_b may not fully overlap and hence the composite automaton would be a partial composition of the T_a and T_b automata.

automatons (including itself) it would always produce itself leading to its certain and complete domination of the population

- Type 1 - a new automaton type was generated from the interaction of two other automatons and was different from T_a and T_b (see Figure 3.4)
- Type 2 - a new automaton was generated from the interaction of two other automatons and was identical to one of them (see Figure 3.5)
- Self-replication - a new automaton was generated where $T_a = T_b = T_c$ (see Figure 3.6)

Automata were categorised based on their number of states ($|Q|$) e.g. one-state, two-state, and so on. The library of one-state automata used in the information niche and computation niche models are shown in their graphical form in Figure 3.7, and the software representation of an automaton is shown in Box 3.1.

Interactions between automata with multiple states ($|Q| > 1$) produced new automata with $|Q_{new}| = |Q| \times |Q|$ states. Given that all automata were required to satisfy the criteria for the class of finite state transducers known as ϵ-machines - thus maintaining the integrity of the automaton types in the population as representing unique, non-duplicated functions - the product automaton (T_c) was further processed in the following sequence [126]:

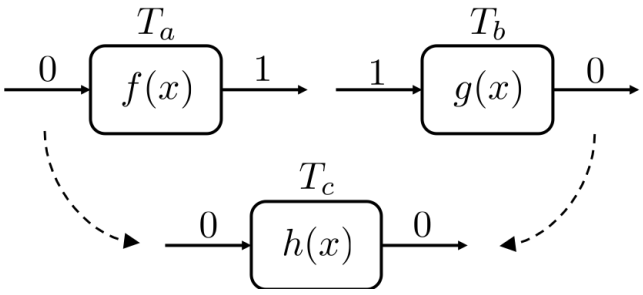

Figure 3.4: Automata could only interact when the range (output) from the first automaton (T_a) was in the domain (input) of the second automaton (T_b). In this example, the output from the first automaton matched the input of the second automaton and hence the interaction was successful. A successful interaction led to the production of a new automaton that inherited the domain of the first automaton (T_a) and the range of the second automaton (T_b) which, in this example, led to the formation of an automaton with a different structure (function) than either of the interacting automata that produced it.

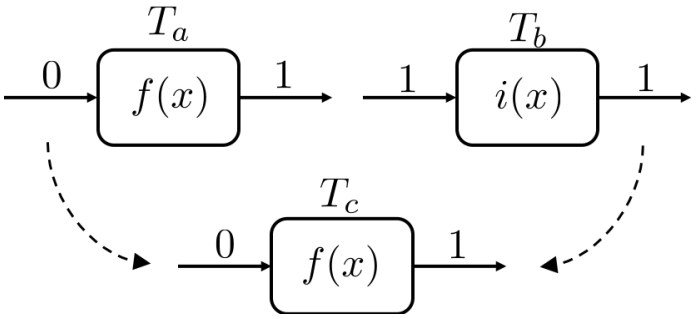

Figure 3.5: Example of the production of a new automata (T_c) where it was identical to T_a or T_b.

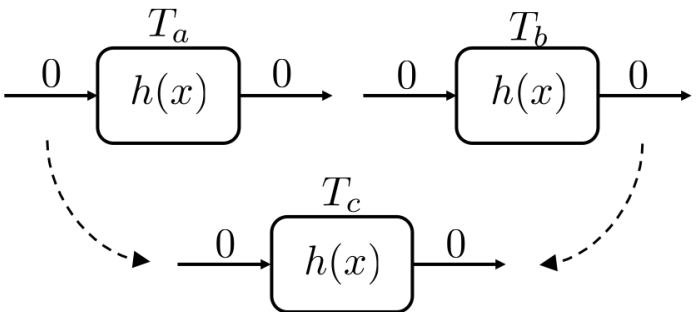

Figure 3.6: Automata could also interact with automata of their own type (i.e. $T_a = T_b$) and for some automaton types this led to self-replication and hence $T_c = T_a = T_b$.

1. all unreachable states of the product automaton (T_c) were removed

2. the automaton was minimised using the Hopcroft algorithm [127] which identified equivalent states and replaced them with a single state leaving an automaton with $|Q_{min}|$ states where $|Q_{min}| \leq |Q_{new}|$

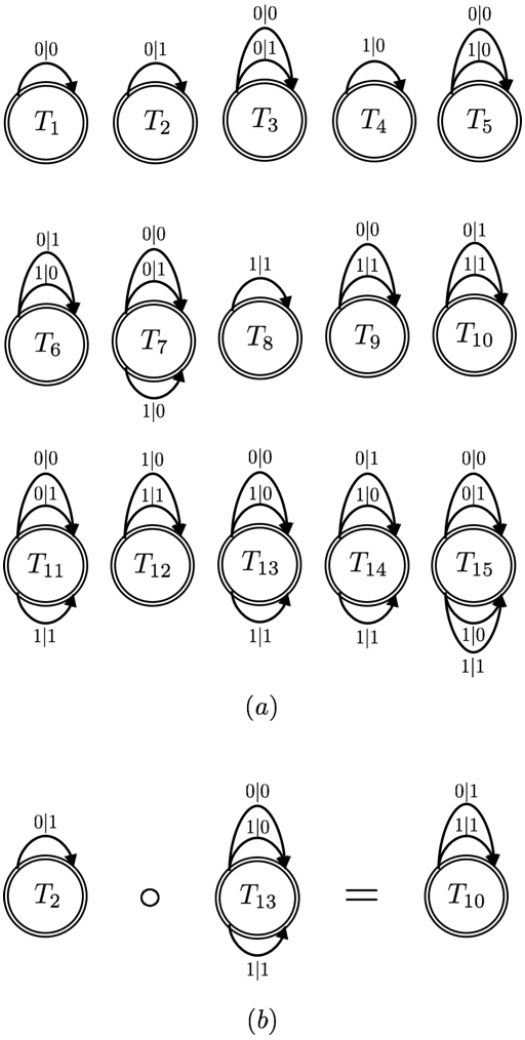

Figure 3.7: (a) Graphical representation of the 15 single-state automaton types (T). The binary numbers on the arrows indicate the state transitions e.g. T_3 accepted only the input symbol '0' which it transformed to either a '0' or '1' output symbol; (b) The functional composition of the automata T_2 and T_{13} in the non-commutative equation $T_2 \circ T_{13}$ (as per $T_b \circ T_a$) to generate the T_{10} automata. T_2 transforms the output from T_{13} which yields the T_{10} automata that takes the input domain from T_{13} and the output range from T_2. There were a total of 207 interactions in this one-state automata library (see Section 3.6.1). Where the domain of a T_b automata did not match any outputs from the T_a automata then the interaction was deemed to be unsuccessful. Taken from [50].

3. validation that the topology of the minimised automaton had at least Q_{min} transitions. Where there are $|Q_{min}| - 1$ transitions then at least one state did not have an outgoing transition and, as such, the automaton was *not* a strongly connected topology and hence failed the ϵ-machine criteria

Not all interactions generated a valid automaton after the above processing had

occurred and these were considered unsuccessful and the product automaton was discarded and no changes were made to the population. Successful productions were those that met the criteria of an ϵ-machine and would consist of $1 \leq \mid Q_{min} \mid \leq \mid Q_{new} \mid$ states. Sometimes new automata introduced new unique functionality into the population. These novel automata were important in examining the dynamics of an open-ended population (see the results of simulations of generating novel automata in Chapter 9). Implementation of the above procedure for minimising and validating new multi-state automata as valid ϵ-machines was computationally expensive and required a parallel processing strategy using the University of Bristol supercomputer "BlueCrystal" (see Appendix 12.1.1 for further information).

In summary, interacting finite state automata produced new automata and the rules governing their interactions as described in this section were implemented consistently in the information niche and computation niche models.

3.3 The Information Niche - a model of a self-producing population

An information niche was the label given to a population of interacting automata that had reached a steady-state composition within an environment. The information niche model consisted of three components: the automata (as described in Section 3.2), the internal environment which was a square lattice with a single automata occupying each lattice site and in which the automata interact and produce new automata (see Section 3.3.1), and an external environment that imposed conditions on the interacting population in two ways: (a) the random replacement of incumbent population automata with a randomly generated automata to simulate the influx of foreign automata into the population, and (b) the random re-location of automata on the lattice to simulate diffusion and spatial mixing (see Section 3.3.2).

3.3.1 Internal Environment

Each of the 15 types of one-state automata (see Figure 3.7) were randomly distributed in equal numbers across a square lattice Γ of $n \times n$ sites where n was the width of the lattice. Each site was occupied by a single automata to give a total population size of $N = n^2$. The lattice was equivalent to a two-dimensional asynchronous cellular automaton (see Box 3.2). The replication of a new automata proceeded by randomly selecting an existing automata T_d from the lattice as a candidate to be replaced by a new automata (T_c). There were two ways in which the T_c automata could be generated: (a) from the functional composition of

two successfully interacting automata (as per the non-commutative equation $T_b \circ T_a = T_c$) that reside on neighbouring sites to T_d (see Figure 3.8), or (b) from the random replacement of T_d with a randomly generated automata (T_c). The probability that T_c was a randomly generated automata or derived from the interactions of two neighbouring automata was given by Φ and $1-\Phi$, respectively where $0 \leq \Phi \leq 1$. The successful production of T_c replaced T_d thus maintaining a constant population size (N). A constant value for N created a selective pressure between automaton types each of which must be continually produced to maintain their presence in the population.

The procedure for producing new automata was iterated from 10^5 to 10^7 time steps (depending on the aims of a particular simulation run) and that led to the growth or decay of particular automaton types (T). This simulated the population dynamics over time and that led to the emergence of a number of distinct information niches. Changes in the structure and composition of the population were observed as the simulation progressed and this was captured at each time step by updating the frequency distribution (f) of the information processing types present in the emerging community. The following difference equation described the rate of change in the concentration of an automaton (f_c) on each time step [123]:

$$\Delta f_c = \left((1-f_c) \sum_{T_b \circ T_a = T_c} f_a f_b\right) - \left(f_c \sum_{\substack{T_b \circ T_a \neq T_c \\ T_b \circ T_a \neq T_0}} f_a f_b\right) \tag{3.1}$$

Where T_a,T_b were the interacting automata, T_c was the new automaton produced from that interaction and f_a, f_b, f_c were their normalised frequencies of occurrence in the population. T_0 was the transitionless automaton that results from an unsuccessful interaction and which was disallowed in the population. This is a rate equation with the first term indicating the growth of T_c and the second term the decay of T_c. Specifically: (i) growth - the probability of adding the automata T_c into the population was equal to the probability of selecting two neighbours T_a and T_b that produced T_c multiplied by the probability that the automata that was being replaced (T_d) was not the same as T_c (as depicted by the $1-f_c$ term); and (ii) decay - the probability of T_c being chosen for replacement (f_c of the second term) and replaced by an automaton that was neither T_c nor T_0.

The frequency distribution of the automaton types in the population could be determined by solving $\Delta f = 0$ for Equation 3.1. Given that only one lattice location was updated on each time step (an asynchronous update - see Box 3.2) and that there were a large number of automata in the population (given by N which had a typical value of 90,000

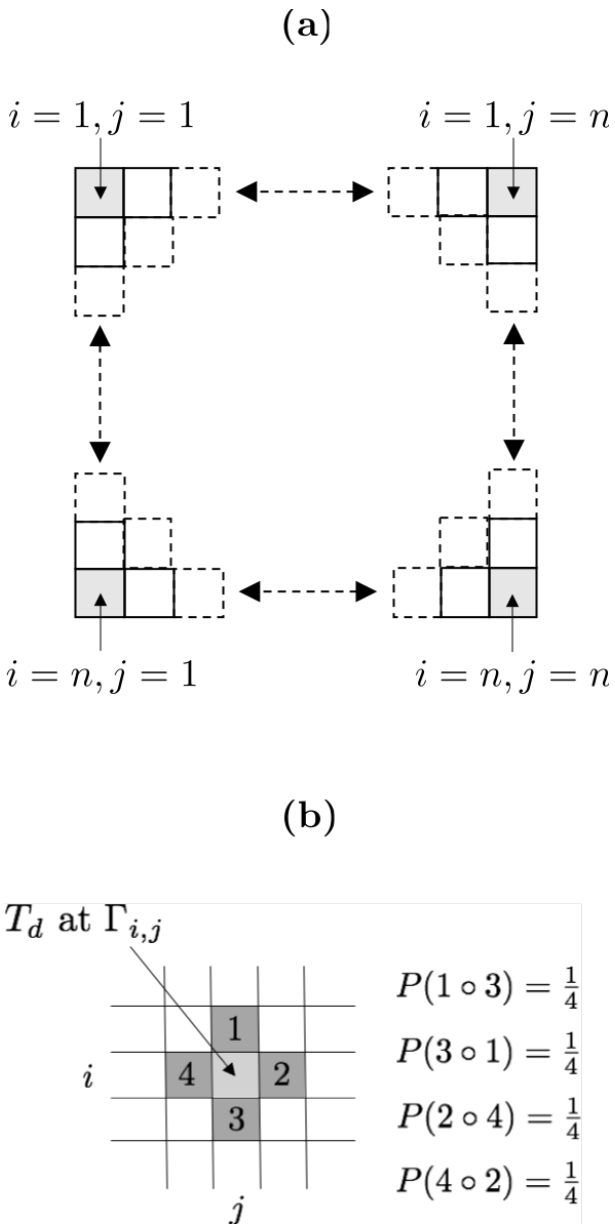

Figure 3.8: The internal environment in which automata interacted was: (a) a square lattice ($\Gamma_{i,j}$) of $n \times n$ sites consisting of a single automata per site. Automata at the boundaries could interact with other automata at the opposite boundary e.g. an automata at lattice site $\Gamma_{1,1}$ (the top-left corner) could interact with automata at the bottom left corner $\Gamma_{n,1}$; and (b) the automata (T_d) on the lattice site $\Gamma_{i,j}$ was chosen at random for replacement by a new automata generated from the interactions of two of its neighbours. An interacting pair were randomly selected from the sites labelled as 1,2,3,4 with the four valid pairings shown e.g. with an equal probability of 1/4 the automata at sites 1 (T_a) and 3 (T_b) could be selected to interact. The functional composition operation would proceed as normal and should a new automata (T_c) be produced then this would replace T_d. Otherwise, T_d would not be replaced and would remain at $\Gamma_{i,j}$. Taken from [50].

for most simulations) this resulted in small changes to the frequency distribution. Hence, discrete time was considered to be a good approximation for continuous time.

3.3.2 Environmental Perturbations

Spatial mixing of automata occurred within the population by randomly selecting a lattice site and exchanging the residing automaton with another type positioned on a different lattice site along one of the cardinal directions at a distance d selected from a one-dimensional Gaussian distribution with variance v and $mean = 0$ and rounding d to the nearest corresponding lattice site. This was repeated for c numbers of different sites per time step. The combination of c and v approximated diffusion such that as $c \to N$ and $v \to n$ the population was considered to be well mixed and, conversely, when $c = 0$ and $v = 0$ the population had zero mobility [123].

Box 3.2 Asynchronous vs. Synchronous Update of the Population

A cellular automaton [128] (CA) is a collection of cells usually arrayed on a grid that can be in one of a number of finite states. Each cell updates its state based on a rule that depends on the states of the neighbouring cells. The dynamics of a CA are generated by repeated application of this local rule by all cells. There are two approaches to updating a CA: "synchronous" whereby all cells are evaluated as per the local rule and the state of each cell is updated accordingly within the same time step; and "asynchronous" where all cells are evaluated successively one after the other i.e. over separate time steps. The appropriate update process to use for modelling a biological process has been investigated and evaluated in terms of 'model stability' [129]. In summary, model stability consists of three considerations: (i) stability of the dynamic system that reaches stable stationary points, (ii) the qualitative behaviour of the model (and its results) do not change significantly if parameters are varied within a certain range, (iii) that the qualitative results of the model are only dependent on the assumptions made about a real biological system i.e. the results are not dependent on how the model has been implemented, for example, whether as a numerical solution of a differential equation or as a cellular automata. Schonfisch & de Roos [129] identified that the two approaches can lead to qualitatively and quantitatively different results in both transient and long-term behaviours of the model with asynchronous updating offering a better approximation of real continuous time. Synchronous updating assumes that all events occur in parallel and, as pointed out by the authors, '... at most points in time and at most places nothing happens' and, as such, a model whereby at most only one event can happen per time step more accurately captures a biological process. The information niche model used the asynchronous update approach.

To simulate the effect of foreign automata entering the population from the environment randomly generated automaton types were allowed to replace randomly selected automata in the population at time t with a probability given by Φ, where $0 \leq \Phi \leq 1$ [36]. With $\Phi = 0$, there was no influx of automata from the environment, no random replacement occurred and therefore changes to the population occurred entirely from the interactions of the existing automata. Whereas with $\Phi = 1$, there was a constant influx of randomly generated automata that were replacing existing automata on each time-step. The combination of the spatial mixing (c, v) and influx rate (Φ) parameters were varied to simulate a range of fixed environmental conditions. The effect of fixed environmental conditions on automata

populations were investigated with a one-state automata population (see Chapters 4 and 6) and a two-state automata population (see Chapter 5).

The effect of intermittent changes to the environment parameters on the robustness of the population was also investigated. For this, changes to environmental conditions could be made once a steady-state population (niche) had emerged:

(i) set the spatial mixing parameters to their opposite value e.g. if a niche had formed in a well-mixed environment then set the spatial mixing parameters to simulate a zero-diffusivity environment e.g. $c = 0, v = 0$

(ii) set the influx rate to its opposite value e.g. if a niche was produced with $\Phi = 0$ then set the influx rate in the range $0 < \Phi \leq 1$

(iii) effect changes to the environment that correspond to both (i) and (ii) occurring at the same time

These sudden changes to environmental conditions (perturbations) once a niche had formed were allowed to persist for a minimum of 10^6 iterations. This proved a sufficient duration for the population to transform its own composition to a new steady-state that represented a different niche in the environment. Once a new niche had formed then the original environmental conditions were reimposed on the population. Subsequently, either the original niche structure was reproduced or a new niche structure emerged. Such intermittent changes to environmental parameters were simulated for one-state and two-state automata populations (see Chapter 4 and Chapter 5).

3.3.3 Co-Habitation of the Lattice

To further examine population dynamics and the emergent behaviour of more complex populations a one-state automata population and a two-state automata population were combined into a joint population located on a $n \times n$ lattice. The effect of different initial proportions of each population were investigated in three ways:

1. All automaton types from unevolved one-state and two-state population (T), consisting of 15 and 1,873 automaton types respectively for a total of 1,888 types, were considered as a single joint population uniformly distributed across the lattice. The corresponding frequency distribution vector (f) describing this joint and uniform population was given by $f = \{f_i \in T \mid f_i = \frac{1}{|T|}\}$ where $\mid T \mid$ was the length of the set of automaton types. Hence, each automaton in this joint population had an initial normalised frequency of $f_i = 1/1888 = 0.0005$

2. automaton types from evolved one-state and two-state populations (i.e. information niches) were combined into a joint population. The population size varied and was dependent on the number of automata that remained after a niche had formed. Therefore, the automaton types in the joint population was given by $T_{ss} = T_{ss1} + T_{ss2}$ where the subscript ss indicated that the set of automaton types had been drawn from evolved, steady-state populations. The joint population was uniformly distributed across the lattice with the corresponding frequency distribution vector (f_{ss}) given by $f_{ss} = \{f_i \in T_{ss} \mid \frac{1}{|T_{ss}|}\}$

3. As per (2) except that the initial proportions of the one-state and two-state automata matched their distributions in their original niches. As such, the frequency distribution vector was given by $f_{ss} = \{f_i \in T_{ss} \mid \frac{f_i}{Z}\}$ where Z was a normalising factor given by $Z = \sum f_{ss1} + \sum f_{ss2}$ where f_{ss1}, f_{ss2} were the normalised frequency distribution of the steady-state one-state and two-state automata populations respectively. Furthermore, $\mid f_{ss} \mid = \mid f_{ss1} \mid + \mid f_{ss2} \mid$

The evolution of these joint populations was recorded for a minimum of 10^6 time-steps and the population structure was analysed. The results of simulating the co-habitation of these populations is presented in Chapter 7.

3.3.4 Inter-niche Transfer of Automata

To examine the cognition process of an autopoietic system (see Section 2.2.3) a model was developed that allowed a two-state automata population to donate one of its automata to a separate one-state automata population at a rate given by $0 \leq \Phi \leq 1$. This led to the replacement of an existing one-state automaton with the two-state automaton from the donor population with a probability given by Φ. Initially, each population was allowed to evolve to a steady-state before the influx rate was increased $0 \leq \Phi \leq 1$ to allow two-state automata to enter the one-state population. The changes in the structure of the receiving population was recorded throughout the simulations and the results are presented in Chapter 7.

3.4 The Computation Niche - a model of a self-producing population with a membrane

The computation niche was an extension of the information niche model operating under well-mixed conditions with the addition of a membrane component that regulated the

production of new automata. The membrane component consisted of a network of automata over which binary information was transferred. The information received by each automata in the membrane determined whether or not that membrane-based automata 'fires' (i.e. surpasses its activation threshold and emits a binary symbol) thus 'exciting' (i.e. primed and ready to participate in interactions) its equivalent automata type in the internal population. Excited population automata were then available to interact with other excited automaton types. Changes in the internal population were reflected in the weightings over the membrane network which, in turn, influenced which information was transferred between membrane automata (see Section 3.6.2). In this way the combination of the membrane and the internal population was processing information. Indeed, the information processes of storage, modification and transfer were all exhibited and hence the label 'computation niche' was used to describe the model (see Section 3.4.4).

The conceptual motivation for the computation niche model was Luisi's minimal autopoietic cell [6] - see Figure 3.9 and Section 3.6.2 for more detail.

The computation niche model explicitly modelled the three components: an external environment, an information processing membrane and the internal self-producing population. Each of these components will now be described in more detail.

3.4.1 Internal Environment

The internal population of the computation niche was based on a simplified version of the information niche model under well-mixed conditions. As global environmental conditions, such as spatial mixing and an influx of material (automata), were not examined in the computation niche model there was no requirement for a cellular automaton implementation of the population. Instead the interactions in the internal population operated analogous to a well-mixed chemical reactor (i.e. where all interactions were possible).

All possible interactions in the population at time t were determined by the activity of the membrane (see Section 3.4.2) with excited automata interacting with all other excited automata to produce new automata[3]. Interactions proceeded on the assumption that in a well-mixed population all automata were available to each other to interact. For each new automata that was produced an existing automata was randomly selected and removed from the population thus maintaining a constant population size. All possible interactions that could occur were performed within the same time step. This was equivalent to a

[3]An investigation into the effect of making this production step a stochastic process (i.e. possible interactions were subject to a failure rate) demonstrated a delay in the formation of the computation niche but qualitatively produced the same result. As such, a probabilistic aspect to the production of automata in the computation niche model was deemed to be unnecessary and only increased simulation run times.

(a) (b)

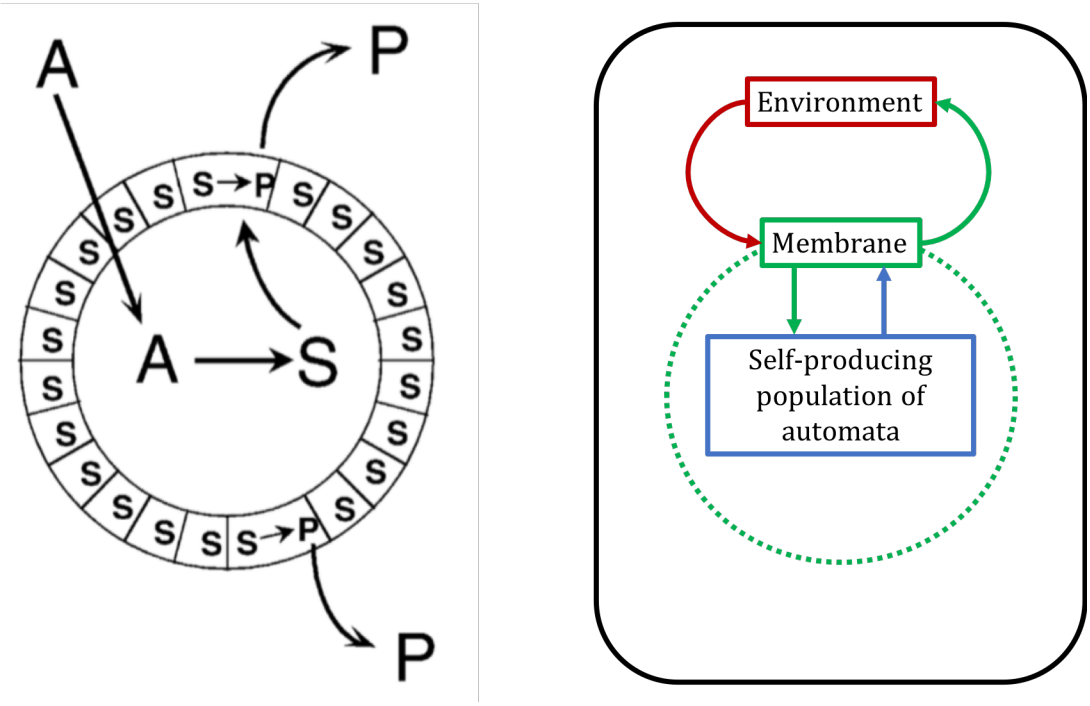

Figure 3.9: The inclusion of a membrane component into the information niche model - aka. the computation niche model - was partly inspired by Luisi's model of a minimal autopoietic unit (a) in that the membrane S was determined by the internal reaction $A \rightarrow S$. The decay of the membrane $S \rightarrow P$ indicated the requirement for continuous renewal of the membrane via. continual production of S. The high level concept of the computation niche (b) was equivalent to this whereby the membrane reflected the productions that occurred in the interior. Furthermore, the membrane acted as the interface between the internal population of interacting automata and the environment. Luisi's model shows the migration of a substrate molecule A through the membrane but does not show any effect of the membrane on this molecule nor on the internal reactions beyond simply acting as a semi-permeable container. The functionality of the membrane in the computation niche is more comprehensive whereby the behaviour of the membrane influences the productions that occur within the interior (green arrow). This is a limitation of the Luisi model and one that the computation niche addresses. Image in (a) taken from [8].

synchronous update of the population on each time-step. As explained in Box 3.2 an asynchronous update method was preferred for emulating biological behaviour in a cellular automaton model however this was deemed less relevant in the computation niche model for two reasons: (i) the well-stirred chemical reaction model used in the internal population of the computation niche was not a cellular automaton; and (ii) repeated simulation runs to test the computation niche model with a one-state population demonstrated qualitatively and quantitatively similar results to a one-state information niche model under well-mixed conditions (see Chapter 8 and Appendix 12.3).

The internal population was quantitatively defined by an interaction matrix (G) and the frequency distribution of the population (f). On each time step the currently active membrane automata (represented by the binary vector Ψ where $\Psi = 0$ and $\Psi = 1$ represented a de-activated and activated automaton respectively) operated on G to temporarily disable parts of the interaction matrix which corresponded with the inactive membrane automata. This led to the inhibition of the interactions involving automata of the same type as the inactive membrane automata and subsequently suppressed the production of the automata that would have been produced from the interactions involving those automata. The interactions that occurred at time t were therefore determined by element-wise multiplication ($\odot$) of the interaction matrix G with the membrane automata status vector Ψ (and where Ψ' was the transpose of that vector):

$$G_\Psi = (\Psi \odot G) \odot \Psi' \tag{3.2}$$

Where G_Ψ was a square matrix of the same dimension as G. The first term yields the product G_{Ψ_i} that sets all elements of a row (i) in G_Ψ to zero where $\Psi_i = 0$; and the second term sets all elements of a column (j) in G_Ψ to zero where $\Psi'_j = 0$.

Where two automata that could interact were (i) active ($\Psi_i = 1$), and (ii) present in the population ($f_i > 0$) a new automaton was produced. The automaton produced was indicated by the value of the interaction matrix element at G_{ij} where i,j were the indices of the two interacting automata (T_a,T_b) respectively. The change in the frequency of automata of type i in the population was determined by:

$$\Delta f_i = \sum\sum f_t \odot A_i \odot f'_t \tag{3.3}$$

Where:

f_t was the normalised frequency distribution of the population in the current time step (as a row vector)

A_i was the adjacency matrix of G^i_Ψ that described all possible interactions that can produce automaton type i

f'_t was the transpose of the frequency distribution vector

Subsequently, the overall change in the frequency distribution of the population was the difference between the frequency of the previous population (F_t) and the changes in the frequency of the population due to new productions (ΔF) to give:

$$f_{t+1} = \frac{F_t + \Delta F}{\sum F_t + \Delta F} \tag{3.4}$$

Where:

F_t was the absolute frequency count of each automata type in the population (as an integer row vector)

ΔF was an integer row vector indicating the absolute change in the frequency of each automata type due to being produced or removed from the population

The divisor was a normalisation factor given as the sum of the updated frequencies of each automaton

f_{t+1} was the normalised frequency distribution of the population

The population's normalised frequency distribution was used to set the weightings of the edges in the membrane network as explained in Section 3.6.2.

When a type of automaton (T_i) was no longer present in the population (i.e. $f_i = 0$) then all interactions with which it was involved were no longer part of the interaction network (G_Ψ) for that time step. When an automaton type was no longer present in the population it was also removed from the membrane. An automaton type that was currently extinct could only be re-introduced into the population and the membrane by being produced by other automata that were present in the population.

3.4.2 Membrane

The membrane was a network of automata that transmitted and received binary information across its own network and exchanged information with an external environment. Conceptually, the membrane separated an internal interacting population (e.g. an information niche) from its environment. The function of the membrane was to process information

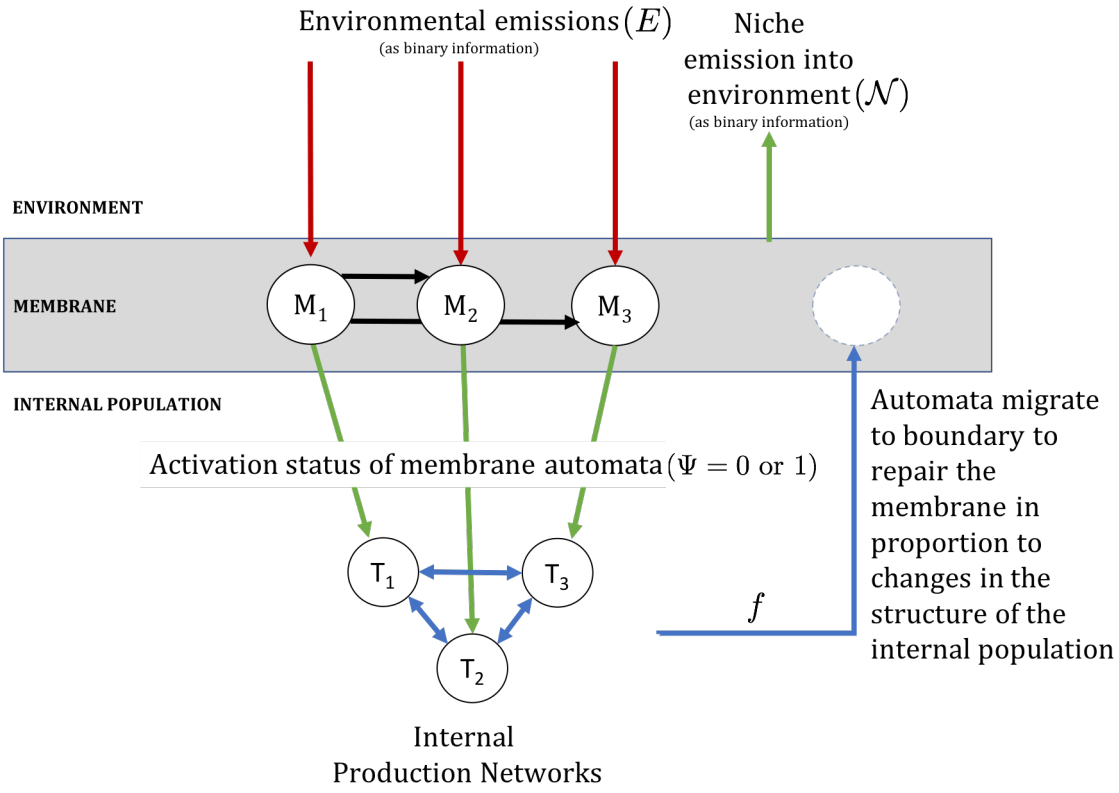

Figure 3.10: The membrane could be visualised as a continuous structure that was embedded with distinct membrane automata (M) each of which had a unique function that reflected the automaton types (T) in the internal, interacting population. Each membrane automata transduces information from the environment and other membrane automata and this sometimes led to emissions that signalled to the internal population which automata were 'on' (excited) or 'off' (inhibited) and able to participate in an interaction to produce a new automaton (a form of top-down causation). This influenced the production of new automata which changed the internal composition of the population which was then reflected in changes to the weighting of edges in the membrane network (a form of bottom-up causation).

from three sources: the environment, from other automata within the membrane, and from the internal population (see Figure 3.10).

The concept of a membrane was inspired by Luisi's model of a minimal autopoietic cell [6] whereby the membrane was produced and maintained by internal reactions. In the Luisi model the membrane contained favourable reactions in the interior which led to the growth and decay of molecules; simultaneously holes appeared in the membrane at a rate consistent with the growth/decay dynamics in the interior. As such, the composition of the membrane in the computation niche model should reflect the changing composition of the internal population of interacting automata. An enhancement on the Luisi model was the influence of an external environment on membrane behaviour and the subsequent effect

that this may have on the interacting population. Any indirect influence that the external environment may have had would be reflected in changes to the internal population structure. This relationship was represented in the membrane as a network with weighted edges between membrane automata where the value of those weightings were directly determined from the population structure. Subsequently, over time and as a simulation progressed the membrane evolved to become a network representation of the internal population of interacting automata and the external environment.

The principles and assumptions behind the design of the membrane were:

1. The automata membrane model is emulating cell signalling [130] i.e. a membrane-bound protein is activated in some manner and either allows small molecules into the interior or transduce information from a membrane-based activity with either event leading to the excitation of a particular molecular species in the interior. In the computation niche model it was assumed that this excitation is of a high fidelity with an extremely low probability of activating non-target automata in the interior. Hence, excited automata in the interior population interacted - under well-mixed conditions - with other excited automata to produce new automata. Within the computation niche model the automata in the membrane automata were assumed to be dormant by default and therefore needed to be triggered in some manner before they excited/inhibited their counterparts in the internal population.

2. To model the maintenance of a membrane from the products of an internal population the membrane itself needed to reflect the composition of the internal population. One option that was considered was that the most populous automata formed the membrane. However simulations of the information niche model demonstrated that the domination of the population by a single type of automata was common and therefore, in the computation niche implementation, this would lead to a homogenous membrane with very limited information processing capacity (i.e. the membrane would only ever represent the behaviour of one automaton type) and, as such, this was dismissed as too limited. The decision was therefore made that the composition of the internal population (i.e. the types of automata present and their relative concentrations) would be accurately represented in the membrane as a network with each automaton type that was present in the internal population represented as a vertex in this network, the interactive relationship $T_a \rightarrow T_b$ would determine the edges between those vertices, and the relative concentration of each automaton type in the internal population would be represented as a weighting over the network edges.

3. The membrane was only a representation of the composition of the internal population. It did not require the removal of any population automata to construct the membrane.

4. Conceptually it was assumed that the membrane consisted of an inert medium that prevented automata in the membrane network from directly interacting with each other to produce new automata. The membrane automata was assumed to be fixed in position and only able to communicate with other membrane automata via. some mode of transferring binary information over their outgoing edges.

5. Changes in composition of the internal population directly affected the behaviour of the membrane due to the change in weightings on the network edges; the implication here was that automata in the membrane needed to be replaced however there were limited positions in the membrane and therefore there was competition within the membrane for occupying space. To reiterate, the number of each automata type in the membrane was proportional to the composition of the population i.e. an increase in the frequency of an automata being produced in the population would increase the weighting given to that automaton's information emissions over the membrane.

6. In the computation niche model the duality of a finite state automata as both function (as an information processor) and reactant (as an interacting entity producing new entities) was represented. Processing of information was performed by the membrane automata. The functional composition of two automata to generate a new automata was performed by the population automata.

7. The membrane model of the computation niche model has a number of conceptual similarities to random boolean networks [131] and neural networks [132] but also important differences. Clarification of such similarities and differences is provided in Box 3.3.

In summary, the membrane was a network of unique and distinct finite state automata that transmitted and received binary information from/to each other over the network edges. The network was derived from the interaction network (as described in Section 3.6.1) and represented the interaction $T_b \circ T_a$ where T_a was the source automaton in the membrane whose emissions were transformed by the target automaton T_b also in the membrane. An edge in the membrane network represented a communication channel between two automaton where the output (y) from the source automaton (T_a) was received by the target automaton (T_b) as an input (x). Each membrane automaton processed the

information it received according to its own unique function which was a property of its internal structure (τ). The automaton T_c which was produced from such an interaction was not represented in the membrane automata as it was already represented in the internal population (see Section 3.4.1).

Box 3.3 Random Boolean Networks and Neural Networks compared to the Computation Niche membrane model

Random Boolean Networks (RBN) are a certain type of discrete, dynamical network that was developed by Stuart Kauffman [131] to model gene regulatory networks. A random boolean network has N vertices in a directed graph where each vertex is either in an ON or OFF state (boolean 1 or 0). Each vertex in a RBN updates its state based on the state values of the vertices which it is connected to on its incoming links. By comparison, the membrane automata in the computation niche model update their state based on the information that is received over their incoming links. This is an important distinction as there are three possible values that are transmitted over incoming links in the computation niche model - a non-communication event represented by an empty set ($\varnothing$) or the transmission of a 0 or a 1 whereas in the random boolean network model there are only two values (0,1).

Artificial Neural Networks (ANN) [132] are a type of computational model that learn (adapt) to perform tasks efficiently and effectively (e.g. image recognition) through modification of the edges of a network towards an optimal configuration. An ANN is a set of connected vertices where each vertex emulates a biological synapse in that they receive, process and transmit signals to other vertices over the edges of the network. Edges are weighted to indicate the strength of the signal between two vertices and are adjusted as learning proceeds. Vertices in an ANN typically have a threshold that the incoming signals must surpass to trigger the vertex to emit a signal over its own output edges. The computation niche model is closely aligned to this concept with a couple of distinctions: (i) information (signals) from the environment are treated as an incoming edge to all membrane automata which is not a feature of an ANN; (ii) each automaton in the membrane network has a distinct information processing function that gives it a unique behaviour in how it responds to information it receives whereas in ANNs the output from vertices are a function of the sum of their inputs - the edge weightings to/from a vertex distinguish their behaviour. In the computation niche the edge weightings and the unique function of the vertex contribute to their behaviour. These are important differences as (i) allows the behaviour of a learning component (i.e. the membrane) to incorporate changes in its environment into the adaptations that are occurring within the network, and (ii) unlocks the ability to analyse the effect of the different information processing behaviour of the membrane automata may have on the systems ability to adapt.

This information processing either led to the membrane automata (M_i) activating ($\Psi_i = 1$) if a certain probabilistic threshold was reached otherwise the automata remained inactive ($\Psi_i = 0$). An activated membrane automata: (a) emitted information (Y_i) corresponding to the processing that it had performed and this was transmitted over its outgoing edges to other automata in the membrane network, and (b) excited its equivalent automata type (T_i) in the internal population so that they were available for interacting with other excited population automata. The membrane automata that were receiving emissions from activated automata treated the incoming information as one of a number of simultaneous information sources from the environment (E) and the emissions from other membrane automata (Y). As such whether a membrane automata activated or not (it's behaviour) was a function of the cumulative information it received from these information sources and its subsequent processing of that information. If a membrane automata wasn't activated ($\Psi = 0$) then it did not transmit information to other membrane automata ($Y_i = \emptyset$) nor did it excite its equivalent automaton types in the internal population.

The effect of this on/off switching of membrane automata excited or inhibited interactions in the population (a form of top-down causation) and to increase/decrease the activation threshold of other membrane automata (a form of same-level causation). The cumulative emissions from all activated automata were emitted into the environment as a two-element probability distribution where it had the potential to modulate environmental information (given by the out-flux parameter Φ_{out} where $0 \leq \Phi_{out} \leq 1$). This in turn could affect the activity of the membrane (a form of bottom-up causation). Hence, the computation niche was modelling hierarchical causation as the information flows between three components - the environment, the membrane, and the internal population of interacting automata.

Figure 3.11 is an illustrative example of a membrane. The information processing functions of four one-state automata are shown (M_1,M_2,M_4,M_8) with M_1 and M_8 repeating the information they received whilst M_2 and M_4 modify the information by 'bit flipping'. Where the output from a membrane automaton could be processed by another membrane automaton a directed edge captured the relationship (see Figure 3.11b). The membrane network matrix describing such a network of membrane automata is shown in Figure 3.11c with the corresponding topology shown in Figure 3.11d. An example of the operation of this membrane is described in Table 3.2.

The membrane reflected the composition of the internal population by allocating a real numbered value (a weighting labelled as λ where $0 \leq \lambda \leq 1$) to each edge in the membrane network. The weighting on each outgoing edge from an automaton was equal to the normalised frequency (i.e. the concentration) of its equivalent automaton type (T_i) in

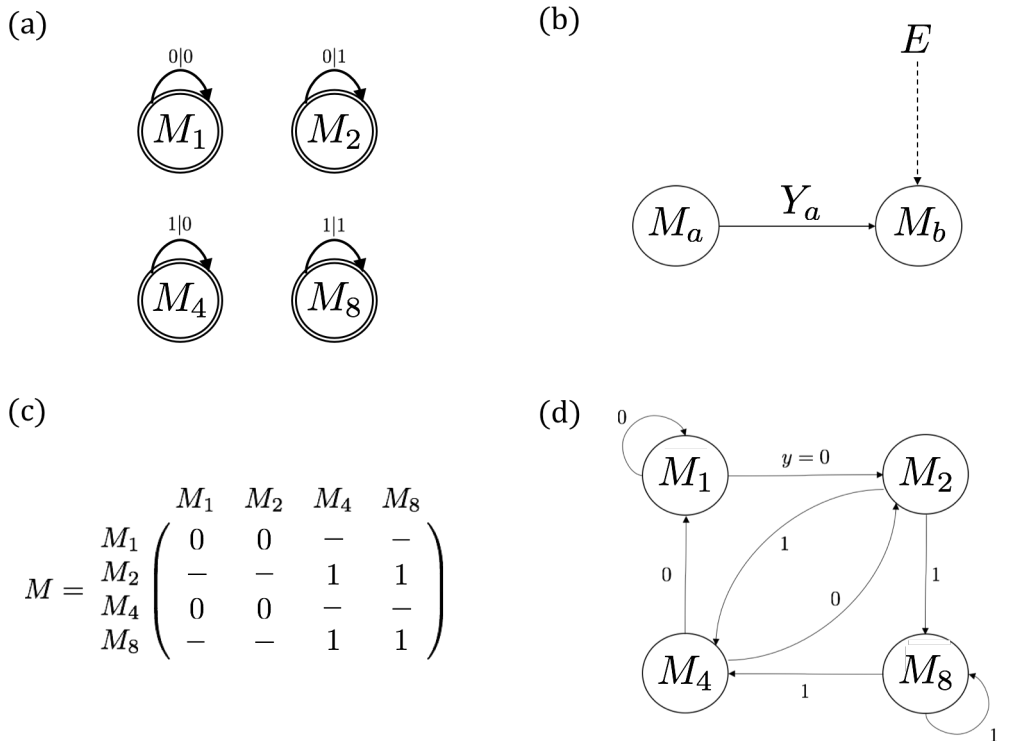

Figure 3.11: Illustrated example of a small membrane network consisting of four automata. The automata are of the same type as used in the information niche model however they are labelled as M_i rather than T_i to distinguish their function in the membrane as processing information rather than interacting to produce new automata: (a) the four membrane automata each of which was a single state information processing transducer that received a single binary symbol and emitted a single binary symbol; (b) the syntax of the membrane network where each vertex in the network represented an automaton type (M_i) and edges between vertices indicated the direction of flow of information e.g. information was emitted (Y_a) from an automaton (M_a) that fulfilled the T_a role in the interaction equation $T_b \circ T_a = T_c$ and which was received by an automaton (M_b) fulfilling the T_b role. All membrane automaton would also simultaneously receive information from the environment (E). All edges in the membrane indicated the automaton types that could interact to produce a new automaton. The automaton T_c produced by the interaction of T_a with T_b was not represented in the membrane network as this would duplicate information already contained in the interaction matrix (G); (c) the membrane network (M) that described the $T_a \rightarrow T_b$ relationships that constituted the membrane network structure where the row headings (i) signified the automaton type acting as T_a and the column headings (j) signified the automaton type acting as T_b in the interaction equation $T_b \circ T_a = T_c$. The value at $M_{i,j}$ was the binary symbol that T_a could transmit and that could be received by T_b and where '-' indicated that no interaction was possible for that T_a, T_b pair; (d) the topology of the membrane automata network with an average degree distribution of 2 with the transmitted symbol labelled on each edge.

t	active	inactive	transmitted symbol	productions
t_0	-	M_1,M_2,M_4,M_8	-	-
t_1	M_1	M_2,M_4,M_8	$M_1 \rightarrow 0$	$1 \times T_1 : T_1 \circ T_1 = T_1$
t_2	M_1,M_2	M_3,M_4	$M_1 \rightarrow 0$, $M_2 \rightarrow 1$	$1 \times T_1 : T_1 \circ T_1 = T_1$ $1 \times T_2 : T_2 \circ T_1 = T_2$
t_3	M_1,M_2,M_4,M_8	-	$M_1 \rightarrow 0$, $M_2 \rightarrow 1$ $M_4 \rightarrow 0$, $M_8 \rightarrow 1$	$2 \times T_1 : T_1 \circ T_1 = T_1, T_4 \circ T_2 = T_1$ $2 \times T_2 : T_2 \circ T_1 = T_2, T_8 \circ T_2 = T_2$ $2 \times T_4 : T_1 \circ T_4 = T_4, T_4 \circ T_8 = T_4$ $2 \times T_8 : T_2 \circ T_4 = T_8, T_8 \circ T_8 = T_8$

Table 3.2: For illustration purposes and assuming no threshold was being applied to the inputs to each membrane automaton: At time-step t_0 all membrane automata were inactive; at time-step t_1, M_1 was spontaneously activated and emitted a '0' symbol over its outgoing edges. As a result it re-activated itself and M_2 which was the only other automaton that could process the binary symbol '0'. At time-step t_2, both M_1 and M_2 are active with M_1 emitting a '0' symbol and thus re-activating itself and M_2 whilst M_2 emitted a '1' which activated the M_4 and M_8 membrane automata. At time-step t_3 all automata were active with M_1 and M_2 emitting information as before and with M_4 and M_8 also now emitting a '0' and a '1' respectively which, in turn, activated all remaining membrane automata. Whilst this information processing was occurring in the membrane, productions in the internal population proceeded in parallel with the creation of a T_1 automaton at time-step t_1 via. self-replication, the automata T_1 and T_2 at time-step t_2, and by time-step t_3 all four automata were being produced in the population. In practice the activation of a membrane automaton was subject to a randomly determined threshold being surpassed meaning that even if an automaton was receiving an input it may not activate. This was a necessary design of the membrane model to prevent self-activating membrane automata such as M_1 and M_8 from being constantly active in the membrane and therefore constantly producing themselves in the population (they are both self-replicators).

the population, hence $\lambda_i = f_i$. Therefore, the cumulative weighting of all outgoing edges from a membrane automaton (M_i) was given by:

$$\lambda_{Y_i} = \sum_{y \in Y_i} f_i \tag{3.5}$$

, where Y_i was the set of all outgoing edges from the membrane automaton M_i. Hence, each outgoing edge had an identical weighting $\lambda_y = f_i$.

For a given membrane automaton (M_i) the cumulative weighting of all incoming edges (X_i) was given by:

$$\lambda_{X_i} = \left(\sum_{x \in X_i} \lambda_x \right) . \frac{1}{Z} \tag{3.6}$$

, where X_i was the set of all incoming edges to M_i, λ_x was the weighting of a single edge (x) in the set X_i, and $Z = \sum \lambda_{X_i}$ (i.e. a normalising factor).

The higher the concentration of a membrane automaton's equivalent population automaton the greater the magnitude of its emissions due to a higher edge weighting (as per

$\lambda_i = f_i$). For the majority of the time emissions of a greater magnitude had more influence on the activation behaviour of the receiving membrane automata [4]. The weighting of edges to match the internal population allowed for changes in the composition of the population to influence information flow in the membrane (a form of bottom-up causation) and, given that information flows contributed to the activation behaviour of membrane automata, also indirectly affected the production dynamics in the internal population (a form of top-down causation) thus closing a causal cycle.

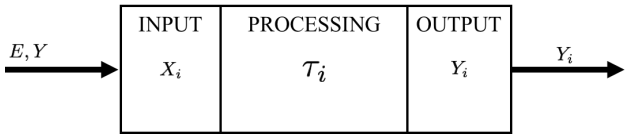

Figure 3.12: Information was received at a membrane automaton's input (X_i) from the environment (E) and connected automata (Y). The information was then processed by the automaton according to its input characteristics (τ) to determine if a threshold had been surpassed that triggered an emission from the automaton (Y_i) which was transmitted to membrane automata over its outgoing edges. The activation status of the automaton was captured in the variable Ψ_i where $\Psi_i = 0$ and $\Psi_i = 1$ represented an inactive or active automaton respectively. Cumulatively the emissions from all activated membrane automata were emitted to the environment as a probability distribution ($\mathcal{N}$) of two events occurring (the probability that the binary symbol '0' or '1' would be emitted from the niche respectively) at an intensity given by Φ_{out} and $0 \leq \Phi_{out} \leq 1$. Each membrane automaton in the membrane therefore acted as an information processing unit that transduced information from incoming communication channels (E,Y) to its outgoing communication channel (Y_i) and modifying that information according to its internal structure.

Figure 3.12 summarises the three information processing steps performed by a membrane automaton. Information could be received from two sources: the environment (E) and other membrane automata (M). The processing of environmental information (E) by membrane automata is explained in Section 3.4.3. Here, the information received (X_i) by a membrane automaton (M_i) from other membrane automata (information from the environment is treated in Section 3.4.3) was given by:

$$X_i(t) = \left(\sum_{x \in X} \lambda_x \right) . \frac{1}{Z} \tag{3.7}$$

Where:

[4] This was not always the case as some membrane automata could transmit more information (e.g. dual output automata that can emit '0' and '1' symbols) in a time-step than automata to which they were connected could process (e.g. mono input automata that could only accept either a '0' or a '1') and, in such circumstances, the magnitude of the emission was irrelevant to the behaviour of such receiving automata.

X_i was a two-element vector that represented the sum of the magnitude of '0' and '1' symbols received on the automaton's incoming edges (normalised such that the sum of the vector was equal to the value 1)

X was the set of all incoming edges to the membrane automaton from one or more automata connected to this automaton (M_i)

x was the information transmitted by an edge in the set X in the form of a two-element probability distribution where $P(x) = P[x = 0, x = 1]$. Hence, if $P(x = 0) = 1$ then $P(x = 1) = 0$ and this would be represented as $x = [1, 0]$ and likewise if $P(x = 1) = 1$ then $P(x = 0) = 0$ and $x = [0, 1]$. If no information had been transmitted on this edge - that is, the source membrane automaton was inactive - then $P(x) = [0, 0]$ or similarly $P(x) = \emptyset$

λ_x was the weighting value of the incoming edge x

Z was a normalisation factor applied to the sum of all the received information in X to ensure that $\sum \mathrm{X}_i = 1$

Some membrane automata could emit a '0' or '1' depending on their information processing capability and such automata could emit information over their outgoing edges that was outside of the domain of automata that they were connected to. For example, the membrane automaton M_{15} (functionally identical to the population automaton T_{15} - see Figure 3.7) could transmit a '0' or a '1' and it was connected to the membrane automaton M_1 which could only receive a '0' symbol. Hence, M_1 could receive transmissions from M_{15} only when the latter was emitting a '0' symbol. As such, it was necessary to filter the incoming information (X_i) by the functional domain of the receiving automaton (M_i) according to:

$$\mathrm{X}_i^{'} = \mathrm{X}_i . \tau_i \tag{3.8}$$

Where $\mathrm{X}_i^{'}$ was the final input signal presented to the automaton M_i represented as a two-element probability distribution where $P(\mathrm{X}_i^{'} = P(x = 0, x = 1)$ and τ_i was the input probability distribution of the automaton that determined whether it could accept a '0' or '1'. This probability distribution was calculated from the number of transitions of the automaton that accepted a '0' and accepted a '1', as follows:

$$\tau_i = \frac{x_0}{x_0 + x_1}, \frac{x_1}{x_0 + x_1} \tag{3.9}$$

Where x_0 was the count of the automaton's transitions that could accept a '0' symbol and x_1 was the count of the automaton's transitions that could accept a '1' symbol. The values x_0 and x_1 were normalised to yield the two-element probability distribution τ_i. For example, the input properties (τ) for each of the four automaton types shown in Figure 3.11a were: $\tau_1 = [1,0]$, $\tau_2 = [1,0]$, $\tau_4 = [0,1]$, $\tau_8 = [0,1]$.

To determine whether the automaton was activated the automaton's activation threshold was generated as the random number r and the following conditional tested:

$$\Psi_i = \begin{cases} 0 \text{ where } P(x=0) \,||\, P(x=1) < r \\ 1 \text{ otherwise} \end{cases}$$

Where Ψ was a binary vector of length $|M|$ and where each element represented whether a membrane automaton M_i was active ($\Psi = 1$) or inactive ($\Psi = 0$) at the present time-step. Hence, Ψ_i was '1' if either $P(x' = 0)$ or $P(x' = 1)$ equalled or surpassed the random threshold r. Where $\Psi_i = 1$ the value for x that exceeded the threshold was taken as the activated transition of the automaton (i.e. either the '0' or the '1' input symbol surpassed the threshold and these would correspond to the state transition in the automata that had the matching input symbol). If either value of x could have surpassed the threshold - for example, in circumstances where the value of r was close to zero - then the transition that the automata would take was determined randomly with equal probability.

When there was more than one possible transition that satisfied the condition (i.e. the current state of an automaton had two transitions $0 \mid 0$ and $0 \mid 1$ for $x = 0$ or $1 \mid 0$ and $1 \mid 1$ for $x = 1$) the transition that was taken was determined with 50/50 chance. In such occurrences a random real number $0 \leq r' \leq 1$ was generated and the following cases examined e.g. in the case where $x = 0$ activated the automaton:

$$r' = \begin{cases} \leq 0.5, \text{ transition } \{0 \mid 0\} \text{ was taken} \\ > 0.5, \text{ transition } \{0 \mid 1\} \text{ was taken} \end{cases}$$

The same conditions applied where the input $x = 1$ activated the automaton. For example, T_7 had three transitions two of which accepted a '0' and the other a '1'. After determining the final input (X') received at T_7's input, the input probability distribution was $P(\mathrm{X}'_{T_7} = \{0.67, 0.33\}$. Hence, where $r = 0.5$ the '0' symbol surpassed the activation threshold and triggered an emission from the automaton. The symbol that was transmitted was determined by the transition taken by the automaton on being activated. Given that there were two possible transitions for the input symbol '0' the transition that was taken was determined randomly with equal probability. The output symbol associated with the

transition that was randomly selected was transmitted over the automaton's outgoing edges.

To recap an activated membrane automaton triggered two events:

(i) an activated membrane automaton emitted information (Y_i) associated with the output symbol of the transition that was executed during the processing of the information it received at its input ($X^{'}$)

(ii) the interacting automata in the population that were of the same type as the activated membrane automaton were available to interact

Population automata triggered by the membrane could only interact with other activated population automata within that time step (as per the procedure described in Section 3.4.1). To summarise, if a membrane automaton was not activated then this had the effect of inhibiting all interactions of its equivalent population automaton in the internal population. Hence, the behaviour of the membrane directly affected the productions that took place in the population for that time step. Changes in the population structure occurred through the creation of new population automata that replaced existing automata (which were removed from the population). This led to changes in the structure of the internal population which led to changes in the edge weightings in the membrane automata network. This subsequently affected the flow of information within the membrane and the subsequent activation of membrane automata in the next time-step ($t+1$). Changes in population structure therefore acted as a form of bottom-up causation on membrane behaviour. The circular relationship between the membrane, the internal population and the environment are illustrated in Figure 3.13 and the algorithm for updating the computation niche is described in Box 3.4.

3.4.3 Environment

The computation niche existed within an environment and the relationship between the two was modelled as an exchange of binary information. The information emitted by the environment was represented as a two-point Bernoulli probability distribution $E = \{P(X=0), P(X=1)\}$ where $P(X=0) = p$ and $P(X=1) = 1-p$ where $0 \leq p \leq 1$. For example, $P(E) = [0.5, 0.5]$ represented an environment that was producing 0's and 1's with equal probability. By comparison, $P(E) = [1, 0]$ was an environment that constantly produced a '0' symbol and $P(E) = [0, 1]$ was an environment that constantly produced a '1' symbol. To consider the most general case of the effect of environmental information on the behaviour of the membrane the probability distribution $P(E)$ was randomly generated

on each iteration i.e. $P(E) = (p, 1-p)$ where p was a randomly generated number in the range $0 \leq p \leq 1$. Every membrane automaton had an incoming edge which represented the information being received from the environment. As such, each automaton received information from at least two sources - the environment (E) and other membrane automata (Y) - and this constituted a competitive tension between these information sources to influence whether the receiving automaton would activate or not.

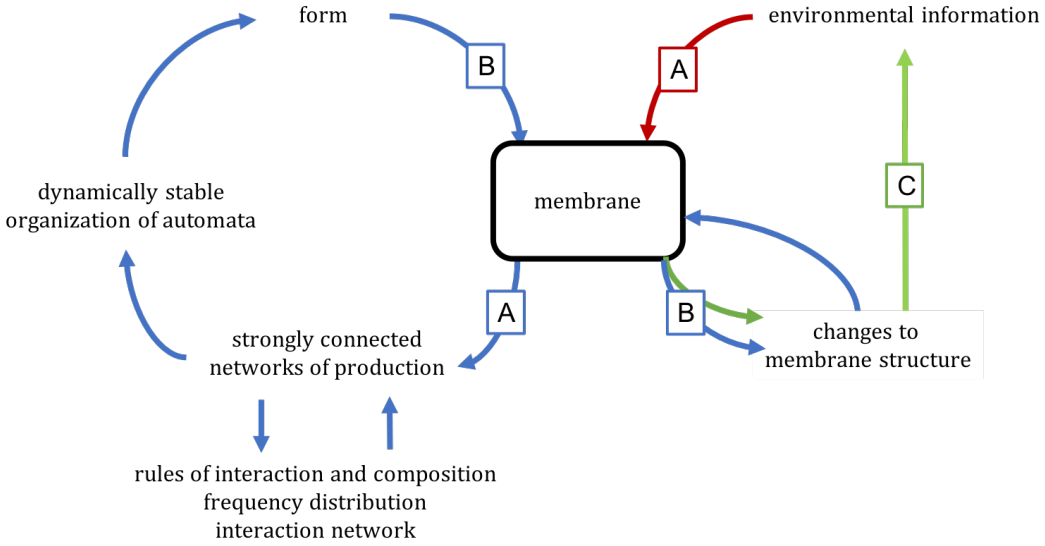

Figure 3.13: The computation niche extended the concept of the information niche to model the relationship between three processes: a self-producing population that was operationally closed (related processes indicated in blue), an environment that was continuously generating binary information (related processes indicated in red), and a membrane that bisected the self-producing population of automata from the environment (related processes indicated in green). The nexus of these processes was the membrane component which changed to reflect both the structure of the population (represented as changes in the weightings over the edges of the membrane network) and the binary information that was being received from the environment at time t. Information from the environment was processed simultaneously by all membrane automata with the effect of inhibiting the production of automata in the population (flows labelled 'A'). Changes in the structure of the population affected the distribution of weights over the membrane network leading to a change in the information processing behaviour of the membrane (flows labelled 'B'). Information generated by emissions of membrane automata were transmitted into the environment subsequently modulating environmental information (the flow labelled 'C').

The calculation for determining the input (X_i') to a membrane automaton was extended to incorporate environmental information:

$$X_i' = (X_i + E) \bullet \tau_i \tag{3.10}$$

Where X_i was the input to a membrane automaton from the aggregation of information received from other membrane automata, τ_i was the input properties of that membrane

automaton, and the environmental information (E) was a two-point probability distribution that was set to various generating modes e.g. E was randomly set to emit '0' or '1' with equal probability or E was set to emit a constant symbol (e.g. a '0' or a '1'). Equation 3.10 combined the two probability distributions (X_i,E) to yield a single probability distribution that represented the total information transmitted to a membrane automaton (M_i). Not all transmitted information could always be read by the receiving automaton and so the probability distribution - that represented the transmitted information - needed to be modified by the input properties of the receiving automaton (τ_i). For example, if the transmitted information probability distribution was $X_i = [0.5, 0.5]$ and yet the receiving automaton could only read 0 symbols - where $tau_i = [1, 0]$) - then ($X_i + E$) would need to be modified by the information processing domain of the receiving membrane automaton (τ_i). Hence, the product X_i' represented the transmitted information that could be read by the receiving membrane automaton. This was an important step as it should not be possible for transmitted information that was outside of the domain of the receiving automaton, to be able to activate it.

Box 3.4 Pseudocode for updating the computation niche model

begin
INPUTS:
M : the set of membrane network vertices
f : frequency distribution of the internal population
G : the interaction matrix of the internal population
Y : the set of incoming edges to each membrane automaton
λ : the weightings of each edge in Y
OUTPUTS:
updated f, λ
UPDATE PROCEDURE:
for each i in M
comment: Determine input X_i to membrane automaton M_i
for each y in Y
$R = y \bullet \lambda_y$
comment: Filter input based on automaton's processing behaviour
$R = R \bullet \tau_i$
comment: Determine if membrane automaton is activated
r : randomly generated real number $(0 \leq r \leq 1)$
if $R > r$
comment: Membrane automaton has been activated
$\Psi_i = 1$
fi
end
comment: Produce new automata in the internal population
for each i in $\Psi > 0$
$G_\Psi = \Psi \bullet G_i \bullet \Psi^T$
for each automaton j in G_Ψ
comment: Create new population automaton of type j
$f_j = f_j + 1$
comment: Remove randomly select automaton (d) from population
$f_d = f_d - 1$
end
comment: Update membrane to reflect changes in population structure
$\lambda = f$

Sudden changes to the mode of generation of environmental information acted as a form of perturbation on the membrane. Each vertex in the membrane received the same information simultaneously from the environment and was treated as an incoming edge. Similarly, a weighting was given to the environment information-bearing edge which signified the level of influence of environmental information on the activation threshold of a membrane automaton. This parameter was given by Φ_{env} and was analogous to the size of the opening (aperture), or the permeability, of the membrane that determined the amount of environmental information that could enter the membrane. As such with $\Phi_{env} = 1$ the aperture was completely open and the input to a membrane automaton was completely determined by an exogenous information source from the environment. Conversely, with $\Phi_{env} = 0$ the activation of automata was driven entirely by an endogenous flow of information from within the membrane itself.

To examine the effect of structural coupling between the computation niche and the environment two additional attributes were introduced: (a) the cumulative emissions from all active membrane automata (Ψ) at time t were emitted from the niche into the environment ($\mathcal{N}$), and (b) the parameter Φ_{out} (with $0 \leq \Phi_{out} \leq 1$) which represented the magnitude of the effect of the niche emissions on the environment. The niche emission ($\mathcal{N}$) was the normalised output from all membrane automata at time t according to:

$$\mathcal{N} = \left(\sum_{y \in Y} y \right) . \frac{1}{Z} \tag{3.11}$$

Where $\mathcal{N}$ was a two-point probability distribution describing the probability of the niche emitting a '0' or a '1' at that time-step, y was the information emitted from a membrane automaton and Y was the set of all membrane automata emissions and Z was a normalising factor. Figure 3.14 illustrates the cyclical nature of the information flows within the membrane and between the membrane and the environment.

When $\Phi_{out} > 0$ environmental information (E) was modulated by $\mathcal{N}$ according to:

$$E_{t+1} = \Big((1 - \Phi_{out}) E_B + (\mathcal{N} . \Phi_{out}) \Big) . \frac{1}{Z} \tag{3.12}$$

The term E_B was a two-point Bernoulli probability distribution that represented the mode of generating environmental information *in the absence of* any modulation from the niche e.g. a randomly generated stream of binary digits or a constant binary value. Hence, E_B represented a form of background noise in the environment that was being modulated by information flowing from the niche ($\mathcal{N}$). As $\Phi_{out} \rightarrow 0$ environmental

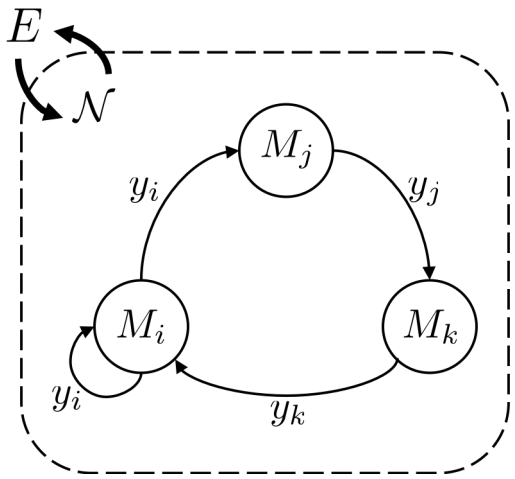

Figure 3.14: There were three types of information flow within the computation niche model: (i) information emitted from membrane automata and received by other automata within the membrane as shown by the y_i, y_j, y_k edges (from the set Y) between the automata M_i, M_j, M_k; (ii) information generated from the environment within that time-step (E_t) and received by all membrane automata simultaneously, and (iii) the aggregation of information generated by all membrane automata that was normalised and emitted ($\mathcal{N}$) into the environment where it potentially modulated environmental information (E). The variable Z was the normalising factor.

information was dominated by this background information source and, conversely, as $\Phi_{out} \rightarrow 1$ environmental information was dominated by the information being produced by the niche ($\mathcal{N}$). In practice, and as discussed in Chapter 8 (the results of simulating the computation niche model) a range of settings for Φ_{out} were examined.

3.4.4 Computation in the niche

The three main elements of the computation niche - the membrane, the internal population of interacting automata and the environment - and the relationships and exchange of information between them have been described. The computation niche model was named as such retrospectively when analysis of the simulation results identified the distributed and intrinsic nature of information processing that was occurring in the model. Specifically, the core elements of computation - information transfer, information storage and information processing - were present and Figure 3.15 illustrates where these processes were manifested in the computation niche model.

As such, the computation niche could be said to be computing (i.e. solving) its own organisation given its present state and that of the environment. Subsequently, a computation niche was defined as a steady-state population of automata that were generated and maintained through the continuous transfer, storage and modification of information that

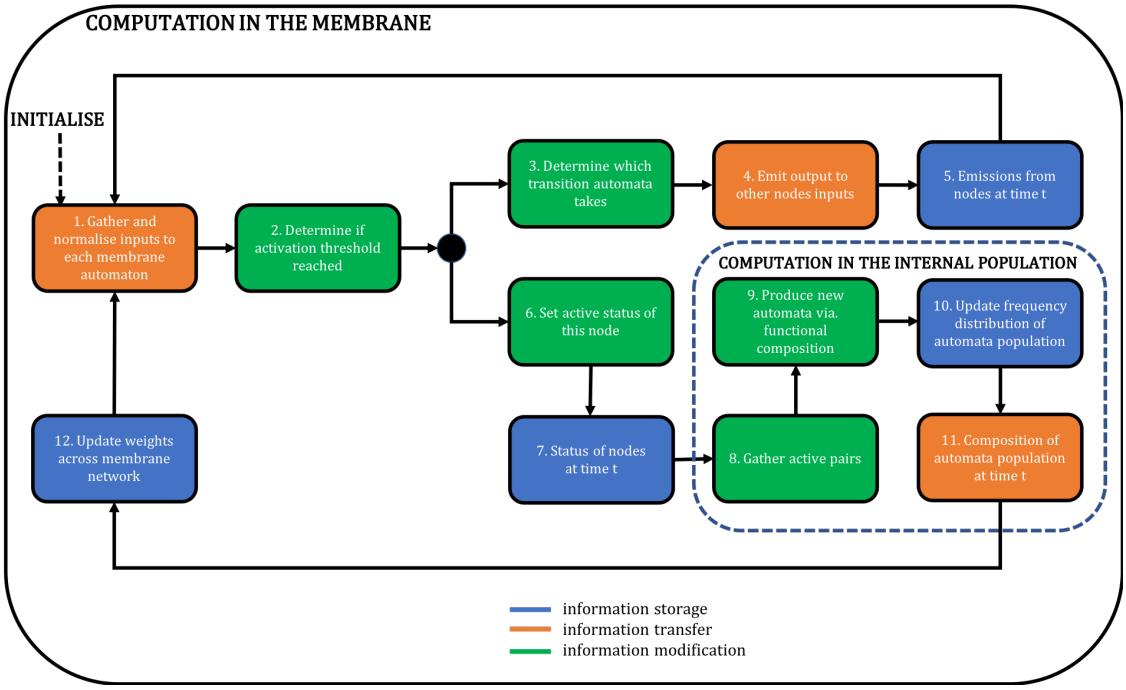

Figure 3.15: A breakdown of one computational cycle in the computation niche that illustrates the type of information processing occurring: information transfer (orange), information storage (blue) and information modification/evaluation (green). The directed arrows show the procedural sequence in which each process was executed.

was an intrinsic property of the production and computation processes occurring between the interacting population, the membrane and the environment.

3.5 Information Measures

This section describes the information measures and methods used to characterise and analyse the results of simulating the information niche and computation niche models. All of the methods described are derived from Claude Shannon's information theory [48] which is the field of study into measuring, storing and transmitting information.

3.5.1 Shannon Information and Shannon Entropy

A key method used in analysing the information and computation niche simulation results was estimating the Shannon entropy [48] of various components and processes of those models. Shannon entropy measured the uncertainty of a system (or, as Cover & Thomas prefer, a random variable [124]) based on the likelihood of events occurring in that system.

In a system each event that could occur contained a certain amount of Shannon information, given by $I(x) = -\log_2 p(x)$, measured in binary digits (bits). Shannon information could be understood as the amount of information that was yielded when that event occurred. The less probable an event the more information it yielded when it did occur [5] and, as such, Shannon's Information was a measure of the degree of surprise - or the amount of uncertainty - we had about an event occurring.

The Shannon information could be calculated for each possible event occurring in a system. For example, on each time step in the information niche model one existing automaton was randomly selected and replaced with a new automaton. In a one-state population at the start of a simulation there were 15 automaton types. At the beginning of a simulation each automaton type was equally distributed and therefore there was a $P(x) = \frac{1}{15}$ chance of an automaton of type x to be selected for replacement by a new automaton. Hence, if automaton x was indeed selected then the Shannon Information that was yielded from this event occurring was $I(x) = -\log_2 . P(x) = -\log_2 . \frac{1}{15} = 3.9$ bits.

The Shannon entropy was the average information that could be yielded from each possible event in the system of interest:

$$H(X) = -\sum_{x \in X} p(x) \log_2 p(x), \tag{3.13}$$

Where $p(x)$ was the probability of event x occurring from the set of all possible events X. Continuing with the example of the random selection and replacement of automata in a uniformly structured one-state population the Shannon entropy was 3.9 bits which was the same as the Shannon information of a single event. This was to be expected as in a uniformly structured population each event was equiprobable. Indeed, a population with equally distributed numbers of automaton types was characterised by an equiprobable distribution of all events occurring and this represented the maximum Shannon entropy of the system [124]. When all events were equally probable there was the greatest uncertainty about which event would occur next (e.g. which automaton type would be selected for removal and replacement from the population). By comparison, and this was universally the case in all of the simulations of the information niche and computation niche model, as the production of new automata and the removal of existing automata proceeded then the initially uniform distribution of automata was broken with some automaton types growing in number whilst others decayed. Therefore, the probability distribution of all

[5] As a simple illustration of this concept consider the following example: the event of not winning the lottery jackpot yields very little information. By comparison, the event that you win the jackpot is a big surprise and conveys more information.

automaton	T_1	T_2	T_3	T_4	T_5	T_6	T_7	T_8	T_9	T_{10}	T_{11}	T_{12}	T_{13}	T_{14}	T_{15}
Frequency distribution of automaton types at $t = 0$ (i.e. uniform)															
$p(x)$	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067	0.067
$I(x)$	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9	3.9
$p(x).I(x)$	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26	0.26
$\sum p(x).I(x)$	$H(X) = 3.9$ bits														
Frequency distribution of automaton types at $t = 10^6$ (i.e. non-uniform)															
$p(x)$	0.069	0.069	0.125	0.069	0.125	0	0	0.069	0	0.125	0	0.125	0	0	0.225
$I(x)$	3.85	3.85	3	3.85	3	0	0	3.85	0	3	0	3	0	0	2.15
$p(x).I(x)$	0.26	0.26	0.37	0.26	0.37	0	0	0.26	0	0.37	0	0.37	0	0	0.48
$\sum p(x).I(x)$	$H(X) = 3$ bits														

Table 3.3: An example of one way in which Shannon entropy was used in the information niche model. Here the normalised frequency distribution, the Shannon information and the Shannon entropy was calculated for a one-state automata population in the information niche model at $t = 1$ where all automaton types were equally distributed and also at $t = 10^6$ where some automata had grown in number and others had decayed or gone extinct.

possible events in the system became non-uniform. The Shannon entropy of a non-uniform distribution of events would always be less than the maximum Shannon entropy as the uncertainty about the next event to occur had been reduced i.e. if automata of type x had grown in number in the population then there was now an increased likelihood that it would be randomly selected to be removed and replaced with a new automaton. Hence, as the information niche and computation niche simulations progressed the initial uniform state of the population became less uniform. The uncertainty about the possible changes that could occur had been decreased as there was increasing structure emerging within the niche. Measuring the Shannon entropy of the normalised frequency distribution of each automaton type in the population provided a quantitative estimate of the structure of the population. For example, consider the worked example in Table 3.3 showing the reduction in Shannon entropy of 3.9 bits when the population was uniformly distributed to 3 bits after significant changes had occurred to the composition of the population.

The Shannon entropy was used in the information niche and computation niche models to:

1. Quantify the complexity of the interaction network that was driving production of new automata (Section 3.5.2)

2. Quantify the minimum information required to generate a niche (Section 3.5.3)

3. Quantify the internal complexity of an automaton (Section 3.5.4).

Each of these measures will now be described.

3.5.2 Interaction Network Complexity

The distribution of automaton types in a given population determined the range of possible interactions. Changes in population structure [6], and the consequent diversity of interactions available, was quantified at each time step using the interaction network complexity ($C_\mu(G)$), which measured the amount of information required to describe the probability that each interaction could occur in the population contingent on the current structure of the population [36]:

$$C_\mu(G) = -\sum_{f_a,f_b,f_c} \frac{v^c_{ab}}{V} \log_2 \frac{v^c_{ab}}{V}, \tag{3.14}$$

where

$$v^c_{ab} = \begin{cases} f_a f_b, & \text{if } T_c = T_b \circ T_a \text{ has occurred} \\ 0, & \text{otherwise.} \end{cases}$$

Where v^c_{ab} was the number of times that automaton type T_c could be produced from the interaction of T_a and T_b, $V = \sum v^c$ was a normalising factor and f_a, f_b were the proportion of automaton types T_a and T_b in the population, respectively. Equation 3.14 determined the likelihood of an interaction occurring to produce T_c given the current composition of the population. Over time changes occurred to the population as some automaton types increased in number whilst some became extinct. Such changes were to the benefit of those automaton types that were growing in number as they were more likely to get selected to participate in future interactions. As only one new automaton could be produced on each iteration, every interaction that could occur was competing with all other potential interactions. Subsequently, the probability of a specific interaction occurring was contrasted against the sum of the probability of all other possible interactions, as given by the normalisation term V. The probability of an interaction occurring to generate a particular automata type was the sum of the normalised frequencies of those automata responsible for its production. This normalised probability was calculated for each automata type in the population to yield a probability distribution. The Shannon entropy of this probability distribution then yielded the interaction network complexity $C_\mu(G)$. Calculating the interaction network complexity provided a quantitative measure of changes in the Shannon entropy of the interaction network.

[6] Population structure and population composition are used interchangeably and both refer to the number of and type of automaton types that are present in the population at a moment in time.

3.5.3 Information Content of a Population

Quantifying the minimum information required for generating a niche (i.e. a steady-state configuration of the population) was undertaken by defining the production threshold as a measure of the information required to describe the minimum number and the type of automata that were required to be produced to create the niche. The production threshold for a niche was determined by calculating the Shannon entropy (H) of the frequency distribution (X) of each automaton type that would need to be produced within a given population:

$$H(X) = -\sum_{i=1}^{|T|} x_i \log_2 x_i, \tag{3.15}$$

where x_i was the proportion of interactions in the population that produced automaton type i and T was the set of all automaton types (and $\mid T \mid$ was the size of that set). The production threshold differed between niches depending on the number of constituent automata, with lower values for those niches in which not all automaton types were present. This measure was used to compare the information required to transition between niches, elucidate how the niches transitioned in response to perturbations in environmental conditions and explain why some niches were more robust than others. In general, the production threshold and interaction network complexity were complementary. The former quantified the information required to generate a niche, whereas the latter quantified the information required to describe a niche after it had evolved to a steady-state distribution, and any interactions that remained between the automata.

3.5.4 Structural Complexity

Given the specific properties of ϵ-machines [133] - on which the interacting automata of the information niche and computation niche models were based - it was possible to quantify the structural complexity of an automata or, more usefully, the "amount of information storage it has" [134] which was given by [135]:

$$C_\mu(T) = -\sum_{\sigma \in \mathscr{S}} P(\sigma) \log_2 P(\sigma), \tag{3.16}$$

where $P(\sigma)$ was the probability distribution over the states ($\mathscr{S}$) of the automaton (i.e. how often they were visited). The structural complexity of an automaton was therefore estimated based on the distribution of probabilities over its internal states. The structural

complexity was calculated for each new novel automata generated in the open-ended population simulations (see Chapter 9).

3.5.5 Information Processing Capacity of Automata

Each automaton had an information processing capacity (ρ) which indicated the domain and range of information that it could process (or, alternatively, the binary symbols that it could receive and transmit) and, therefore, the range of interactions it could have with other automata. The higher the interaction potential of an automaton the more possibilities it had to interact with a wider range of automata either in the role of a T_a or a T_b automaton in the functional composition operation $T_b \circ T_a = T_c$. This was measured directly from the automaton's structure. For example, the one-state automaton T_1 accepted a '0' and emitted a '0' from the alphabet $A = \{0,1\}$ and therefore it had one input channel and one output channel for a total of two channels. Formally this was denoted as the logarithm $\rho(T_1) = \log_2(2) = 1$ bit. By comparison, the one-state automaton T_3 accepted a '0' and emitted a '0' or a '1' for a total of three channels hence $\rho(T_3) = \log_2(3) = 1.6$ bits. The automata in the one-state population were partitioned in this manner to aid in the analysis of their competitive properties (see Section 8.3.4).

3.6 Network Measures

A network [49] was a collection of vertices joined by edges that represented the relationships that existed between automata. An automata was represented as a vertex in all the networks that were generated in the information niche and computation niche models. Two types of network were implemented: the interaction network (G) - see Section 3.3 - that described which automata were produced from the interactions of other automata, and the membrane network ($\mathscr{M}$) - see Section 3.4.2 - which described the order in which automata interacted with each other.

This section describes the methods used to capture the properties of these networks in one-state, two-state and multi-state automata populations.

3.6.1 Interaction Network

The interaction network (G) [36] was a directed graph where vertices represented automaton types and the directed edges indicated that the vertex at the beginning of the edge was T_a and the vertex at the end of the edge was T_c in the functional composition operation $T_b \circ T_a = T_c$ and the labelled edge indicated the automata type T_b that was

transforming the output of the T_a automata to produce the T_c automata. This network was mathematically represented as a $|T| \times |T|$ matrix (where T was the set of all automaton types in the population and $|T|$ was the size of that set) where the rows (i) indicated the T_a automaton types and the columns (j) indicated the T_b automaton types. The value at the intersection of a row and column ($G_{i,j}$) was the index of the automata type that was produced (T_c) by the interaction of T_a and T_b. For example, the automata type T_2 interacting with T_4 creates the automata type T_1 and therefore the matrix entry was $G_{2,4} = 1$ which was represented graphically as shown in Figure 3.16.

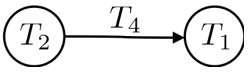

Figure 3.16: An example of the graphical representation of the interaction network (G). The two vertices represent the T_a and T_c automata and the edge label represents the T_b automata in the functional composition equation $T_b \circ T_a = T_c$.

3.6.2 Membrane Network

The membrane network ($\mathscr{M}$) was a directed graph where vertices represented automaton types and the directed edges indicated that the vertex at the beginning of the edge was T_a and the vertex at the end of the edge was T_b in the functional composition operation $T_b \circ T_a = T_c$. The network was mathematically represented as a $|T| \times |T|$ matrix where the rows (i) indicated the T_a automaton types and the columns (j) indicated the T_b automaton types. The intersection of a row and a column ($\mathscr{M}_{i,j}$) indicated the binary symbol that could be transmitted from T_a and received by T_b. This was only the case where the range of the T_a automata type was in the domain of the T_b automata type and therefore the automata type T_b could receive information from T_a. If this was not the case then a null value ($\mathscr{M}_{i,j} = \emptyset$) indicated that these automaton types did not communicate with each other in that particular ordering (the functional composition operation was non-commutative and therefore the ordering of the automaton types could lead to a different outcome). For example, T_2 as T_a and T_1 as T_b could not communicate and therefore $\mathscr{M}_{2,1} = \emptyset$ but they could when T_1 was T_a and T_2 was T_b and therefore $\mathscr{M}_{1,2} = 1$. Figure 3.17 illustrates the graphical representation of the relationship between T_a and T_b automata.

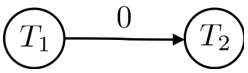

Figure 3.17: An example of the graphical representation of the membrane network ($\mathscr{M}$). The two vertices represent the T_a and T_b automata in the functional composition operation $T_b \circ T_a = T_c$ and the edge label represents the binary symbol that was transmitted from T_a to T_b.

3.6.3 Topology and Degree Distribution

The general properties of the interaction network (G) that represented the productions within the automata population were characterised as (i) the number of vertices and edges within the network, and (ii) the degree distribution of those edges [49].

The number of vertices in the network at time t was calculated from examination of the interaction network matrix. Where $G_{i,-} \neq \emptyset$ (the automata acted as a T_a automaton in at least one interaction that produces a new automata) or $G_{-,i} \neq \emptyset$ (the automata acts as a T_b automaton in at least one successful interaction that produces a new automata) and $f_i > 0$ (the automata exists in the population) the automata was deemed to exist in the population, and to be available to interact with other automata, and therefore was part of the topology of the interaction network.

The degree of a vertex (k) in the network was the number of edges it had to other vertices - both incoming and outgoing edges - and the degree distribution ($P(k)$) was the probability distribution of those degrees over the network i.e. the fraction of vertices in the network with a degree of k. Subsequently, with v the total number of vertices in the network, v_k the number of vertices with a degree k then the probability of a vertex with a degree of k occurring in the network was given by $P(k) = \frac{v_k}{v}$. The degree distribution revealed the structure of the network e.g. a network with a long tail degree distribution [136] indicated that there were a very few, highly connected vertices with the majority of the remaining vertices in the network significantly less well connected and, by comparison, a network with a very narrow degree distribution indicated a highly connected network with a more symmetric topology.

The topology and the degree distribution of the interaction network was examined in one-state (see Chapter 4), two-state (see Chapter 5), multi-state (see Chapter 9) and joint one/two-state automata populations (see Chapter 7).

3.6.4 Detecting strongly connected networks

Self-organising behaviour has been linked to positive feedback loops in a system [137] which in a network topology is recognised as a strongly connected component [138]. For directed networks that are describing reactions/interactions such structural motifs indicate the presence of reciprocation and mutual production [139]. There are a significant number of different interaction sub-networks in a one-state automata population and so an algorithm was developed to detect structures in the interaction network (G) that had the motif of a strongly connected component (see Box 3.5).

Box 3.5 Pseudocode for identifying strongly connected interaction networks

```
begin
  W : The set of all possible combinations of sub-networks
  for each w in W
      create adjacency matrix A for w
      where A_i are outgoing edges and A_j are incoming edges
      if SUM(A_i) ≥ 2 AND SUM(A_j) ≥ 2 for EACH vertex in w
      then add w to S
  end
```

This was an exhaustive algorithm that examined all possible combinations (W) of automata interactions partitioned into many sub-networks (w) ranging in size from two to 15 automaton types. For each possible sub-network (w) an adjacency matrix (A) was generated that defined the topology of the network as a directed graph [49]. The vertices represented individual automaton types and the edges signified the interactions that could occur to generate new automaton types within that network. The structure of A was tested for mutual production where: (i) A had a minimum in-degree of two edges, and (ii) a minimum out-degree of two edges[7] This implied that the automata in the network produced at least one other automata (excluding self-replication) within the same sub-network. A sub-network was considered to be a candidate for a strongly connected network (S) only if all of its constituent automata met this criteria.

3.6.5 Examining the dynamic stability of an interaction network

Dynamically stable networks were deemed to be those that could continually produce their constituent components without any going extinct (due to other automata being over-produced) and that did not generate novel automata. A numerical simulation of Equation 3.1 was developed to examine the dynamic stability of the strongly connected networks (S) that had been detected in the interaction network (G). The algorithm - which was implemented in MATLAB - is shown in Box 3.6.

[7]Two edges are required to describe a single interaction. Therefore, a minimum in-degree of two was required to denote that the automata represented by a vertex was produced. A minimum out-degree of two was required as each automata in the network must produce at least one other automata apart from itself.

Box 3.6 Pseudocode for testing the dynamic stability of an interaction network

```
begin
  T : the set of automata in the population
  S : the strongly connected interaction matrix that produced automaton i
  f : the normalised frequency vector of all automata in the population
  Z : number of iterations of the simulation
  comment: Run the numerical simulation
  while z < Z
      for each T_i in S
          comment: Calculate changes in frequency of each automaton
          f_i = (f.S_i).f^T
          if f_i = 0
            comment: Loss of this automaton - network deemed unstable
          end
```

The value for Z was determined from performing several test runs of the numerical simulation. Typically a network's stability could be determined within 10^4 iterations. The value for Z used to analyse the networks of the information niche and computation niche simulation results was set at 10^6.

3.6.6 Identifying and counting the unique states of the membrane network

Analysis of the activation history of the membrane's automata identified all of the unique states that the membrane occupied during a simulation. A state here was defined as a unique configuration of the activation status (i.e. active or inactive) of the membrane automata recorded in the vector Ψ. An algorithm was developed to examine the time-series data of the membrane automata activation status $\overleftarrow{\Psi}$ which had been recorded on each iteration of the simulation ($|\overleftarrow{\Psi}| = Z$ where Z was the number of iterations of the simulation) - see Box 3.7.

Box 3.7 Pseudocode for identifying the unique states of the membrane network

begin
$\overleftarrow{\Psi}$: the history (of length Z) of the activation status of each membrane automaton
Ψ_z : the activation status of each membrane automaton at a given point (z) in history
Σ : the unique states of the membrane network that have been identified
s : a specific state of the membrane network
Ω : the counted observations of a membrane network state in $\overleftarrow{\Psi}$
comment: Work through the history of the network membrane states
for each Ψ_z in $\overleftarrow{\Psi}$
find Ψ_z in Σ
if found
comment: A previously discovered network state observed again
$\Omega_s + 1$
else
comment: A new network state discovered
$i = |\Sigma| + 1$
$\Sigma_i = \Psi_z$
$\Omega_s = 1$
end

This algorithm examined the activation history of the membrane and identified each unique state that the membrane entered and how often it entered that state during the simulation. Where:

Σ was a matrix where each row was a unique state of the membrane network (s) and each column represented the activation status of each membrane automaton (M) in that state.

Ω was a $1 \times |\Sigma_{all,-}|$ vector where each Ω_i represented the counted observations of a membrane network state in $\overleftarrow{\Psi}$.

The algorithm proceeds by examining the activation status of each membrane automaton at a specified point (z) in history. The collective status of all membrane automata represents a state of the membrane (s) and each unique state is stored in Σ. As the history of each membrane automaton's activation status is examined the algorithm checks to see if the configuration of membrane activation status has been seen before or whether a new state of the membrane has been found. If the former, then the membrane has re-visited a prior state and this is recorded in the variable Ω_s. If the latter, then the membrane has

entered a new state and this is added to Σ. Hence, on completion of this algorithm the number of unique states that the membrane network occupied during the simulation was given by $|\Sigma|$ and the number of times that the membrane network visited those state was given by Ω. The Shannon entropy of the rate of occurrence of each network state $H(\Omega_{norm})$ was calculated from the normalised form of Ω.

3.7 Summary

This chapter has introduced the concepts of the information niche and the computation niche as complementary models of self-organising populations that examine the two core processes of autopoiesis and cognition under a range of various and varying environmental conditions. The methods for identifying and measuring the emergent properties of these systems has also been discussed. Each Results chapter begins with an explanation of how the simulation of the information niche or computation niche model was set-up to generate the results that are discussed.

CHAPTER 4

RESULTS I - ONE-STATE INFORMATION NICHES

4.1 Reproduction of published paper: Emergence and Dynamics of Self-Producing Information Niches as a Step Towards Pre-Evolutionary Organization

Chapter 4 is a reproduction of the published paper, "Emergence and Dynamics of Self-Producing Information Niches as a Step Towards Pre-Evolutionary Organization" [50] in the Royal Society Interface journal. Reproduced with permission. The full citation is:

Emergence and dynamics of self-producing information niches as a step towards pre-evolutionary organization
Richard J. Carter, Karoline Wiesner, Stephen Mann
J. R. Soc. Interface 2018 15 20170807;
DOI: 10.1098/rsif.2017.0807.
Published 17 January 2018.

This paper describes the key properties of proto-autopoietic organisations that emerged from simulating a one-state automata population evolving under the influence of fixed and intermittent environmental conditions. The main contribution that this paper makes to the field of autopoiesis are:

1. the proto-autopoietic organisations that emerge and that are analysed and quantified

are formed from very simple conditions. As such, this result demonstrates that the basic properties of self-production and robustness required for an autopoietic system can be formed from minimal beginnings. This is an area of autopoietic research that has traditionally been under-developed.

2. the notion of an information niche is introduced to the field of autopoiesis as a particular instance of a proto-autopoietic system as a dynamically stable strongly connected network of mutually producing automata that form distinct organisational steady states under various environmental conditions and perturbations. Critically it was discovered that information can be lost or gained during a perturbation and, in some cases, this leaves the system unable to transform itself back to a prior configuration state. The environment can play the role of adding the necessary information back into the population in the form of a perturbation which proves sufficient for the population to transform to prior states. These findings extend our understanding of the role of an environment in the formation and persistence of autopoietic-like organisations.

The paper is based on the information niche model and made use of most of the information and network measures described in Chapter 3. My contribution to this paper was the implementation and development of the enhancements to the Finitary Process Soup, the design and running of all simulations, and the analysis of the simulation results. The citation numbering used in this publication relate only to those included at the end of the paper. They do not match the citation numbering used in the rest of this thesis.

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Emergence and dynamics of self-producing information niches as a step towards pre-evolutionary organization

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As a step towards understanding pre-evolutionary organization in non-genetic systems, we develop a model to investigate the emergence and dynamics of proto-autopoietic networks in an interacting population of simple information processing entities (automata). Our simulations indicate that dynamically stable strongly connected networks of mutually producing communication channels emerge under specific environmental conditions. We refer to these distinct organizational steady states as *information niches*. In each case, we measure the information content by the Shannon entropy, and determine the fitness landscape, robustness and transition pathways for information niches subjected to intermittent environmental perturbations under non-evolutionary conditions. By determining the information required to generate each niche, we show that niche transitions are only allowed if accompanied by an equal or increased level of information production that arises internally or via environmental perturbations that serve as an exogenous source of population diversification. Overall, our simulations show how proto-autopoietic networks of basic information processors form and compete, and under what conditions they persist over time or go extinct. These findings may be relevant to understanding how inanimate systems such as chemically communicating protocells can initiate the transition to living matter prior to the onset of contemporary evolutionary and genetic mechanisms.

1. Introduction

Theoretical models that attempt to distinguish living from non-living systems, such as Gànti's chemoton [1,2] and Eigen & Schuster's hypercycles [3], assume the presence of replicative molecular machinery, and are constrained in their outlook as they exclude the possibility of protolife behaviour under non-replicative, non-evolutionary conditions [4]. By comparison, the theory of autopoiesis [5] postulates that a living system is distinguished by an ability to continually produce and maintain itself. As these systems properties are not necessarily contingent on the presence of a functioning genetic apparatus, the study of autopoiesis may be critical not only for understanding the transition from (geo)chemistry to protobiology on a pre-Darwinian/pre-genetic early Earth [6] but also for the laboratory-based bottom-up design and construction of synthetic cellularity [7]. Previous computational models of autopoiesis have demonstrated properties such as spatial boundary formation and self-repair in artificial chemistry systems [8–10], but a major limitation of these simulations is their reliance on the pre-existence of an ideal chemistry. While these abstract models have helped to demonstrate the concept of autopoiesis, they do not address how such chemistries come into existence, persist or compete for space, materials and energy under complex reaction conditions. In contrast, other models of autopoiesis such as algorithmic chemistry [11], algebraic chemistry [12] and matrix chemistry [13] do not specify

an ideal chemistry but model the production of interacting entities to simulate the spontaneous formation of higher levels of organization.

In recent years, an alternative prebiotic evolutionary model, termed the finitary process soup [14], has been advanced. It is a model based on binary communication channels and their interaction. The channels take a single bit as input and produce a single bit as output. Since there is no stochasticity, these are deterministic input–output automata [15]. Reproduction, in this model, is represented as an interaction between two automata, with the potential of producing a new automaton. Crutchfield and Gornerup [14,16] present a detailed analysis of the structure and dynamics of this 'soup' of interacting automata. Interestingly, in this model, the emergence of higher level organization occurs spontaneously. Out of an initial set of 15 automata, subsets (networks) of mutually producing automata emerge. These automata networks (also called meta-machines) can be considered as self-producing, autonomous information processing entities. As such, the finitary process soup model represents a basic mechanism for the emergence of autopoiesis in an interacting population. While these findings contribute to the exploration of viable pathways to autopoiesis, they do not specifically pursue the question of how these networks form and compete, and why some networks persist over time while others go extinct.

In this paper, we extend the finitary process soup model to investigate the emergence of steady-state production networks under fixed or intermittent environmental conditions generated by changes in the degree of mixing within and influx rate into an interacting closed population of single-state automata. We find that different environmental conditions lead to different stable combinations, or networks, of mutually producing automata. We call these networks information niches, and we study their specific structural and dynamical properties. The model shows a variety of behaviour, from a small subset of mutually producing automata to a hierarchical network of automata maintaining a stable population. This is quite surprising, given that the model includes only the simplest types of input–output automata.

Furthermore, we investigated the population of automata under sudden environmental perturbations. We observed the emergence of a fitness landscape in which information niches are stable points, which the system can switch between upon perturbation. These results show how proto-autopoietic networks of basic information processors form and compete, and under what conditions they persist over time or go extinct. Thus, our model represents a mechanism for the formation of fitness landscapes under non-evolutionary conditions. These findings may be relevant to understanding how inanimate systems such as chemically communicating protocells can initiate the transition to living matter prior to the onset of contemporary evolutionary and genetic mechanisms.

2. Computational model and methods

2.1. Dynamics of information niches under fixed or intermittent environmental conditions

We employed a previously described computational model [14] to investigate the emergence of steady-state interacting networks and their mutual dependency within a population of interacting/replicating information processing automata. The initial population consisted of 15 types (T_1 to T_{15}) of single-state automata that act as selective communication channels capable of receiving information from a binary alphabet ($A = \{0,1\}$), processing the inputs using between one and four switching/non-switching binary transitions, and emitting the corresponding output in the form of a functional composition in which the sequential processing of the output from one automaton acts as the input for another (figure 1). In the original studies [14], these input–output automata were treated as a special category of finite-state transducers referred to as ε-machines.

Significantly, the replicating population was compositionally closed because the binary interactions between various single-state automata were unable to generate information communication channels outside the original set of 15 members.

An environmental context was imposed on the interacting automata by initially distributing equal numbers of the 15 types randomly across a square lattice Γ of $n \times n$ sites with each site occupied by an individual single-state automaton to give a population size of $N = n^2 = 90\,000$, which was then replicated iteratively using functional composition (figure 1*b*). The production of automata proceeded by randomly selecting a lattice site $\Gamma_{i,j}$ whose occupying automaton (T_d) may or may not be replaced by a new type T_c depending on the competition between the environmental influx and internal production dynamics (figure 2). The probabilities that T_c is a randomly generated automaton entering from the external environment or alternatively derived from the functional composition of two neighbouring automata were given by Φ and $1 - \Phi$, respectively. Production of T_c by either option replaced T_d, which was subsequently removed from the population to maintain a constant value for N. This constraint generated a survival selective pressure between different types of automata, which must be continually produced to prevent depletion from the population.

The production process was iterated for up to 1×10^7 time steps to simulate the emergence of a number of distinct information niches. Changes in the structure and composition of the population were observed with increasing numbers of iterations, and this was captured at each time step by updating the frequency distribution (f) of the information processing types present in the emerging community. The following differential equation described the changes in f on each time step [17]:

$$\frac{\mathrm{d}f_c}{\mathrm{d}t} = (1 - f_c) \sum_{T_a \circ T_b = T_c} f_a f_b - f_c \sum_{\substack{T_a \circ T_b \neq T_c \\ T_a \circ T_b \neq T_0}} f_a f_b, \qquad (2.1)$$

where T_a,T_b are the interacting machines, T_c is the new automaton produced from that interaction and f_a, f_b, f_c are their normalized frequencies of occurrence in the population. T_0 is the transitionless automaton that represented an unsuccessful interaction and was prohibited in the population. Equation (2.1) determines two factors: (i) the probability of adding the automaton T_c is equal to the probability of selecting two neighbours T_a and T_b that produce T_c multiplied by the probability that the automaton that is being replaced (T_d) is not the same as T_c and (ii) the probability of neither T_c nor T_0 being produced. The invariant frequency distribution of machine types can therefore be determined by solving $\mathrm{d}f/\mathrm{d}t = 0$. Here, discrete time is a good approximation for continuous time as only one lattice location is updated on each time step and so for large N (our minimum value for N is 90 000) this leads to a small change in the overall frequency distribution of all

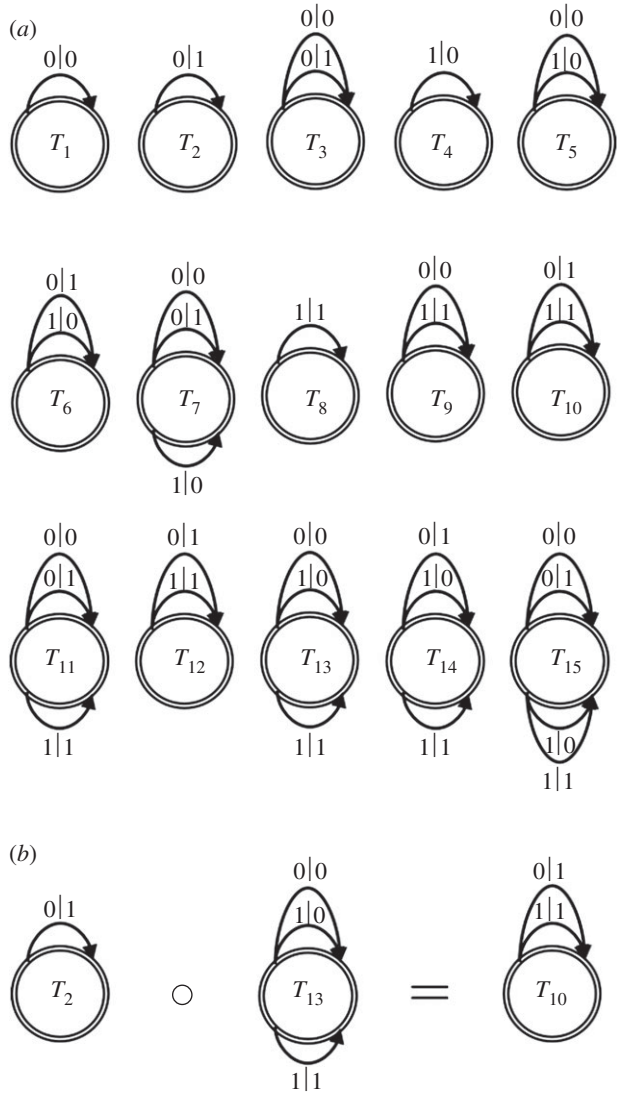

Figure 1. (*a*) Schematic representation showing a compositionally closed population of 15 types of single-state automata (*T*). The population includes four members that are capable of only one transition (T_1, T_2, T_4, T_8), along with six (T_3, T_5, T_6, T_9, T_{10}, T_{12}), four (T_7, T_{11}, T_{13}, T_{14}) and one (T_{15}) that exhibit two, three and four transitions, respectively. The binary numbers on the curved arrows on the top or bottom of the circles indicate the various possible transitions; for example, T_3 operates only with an input signal of 0, transducing this to either 0 (non-switched output) or 1 (switched output) with 50% probability in each case. (*b*) Scheme showing an example of the functional composition of two machines (described by the non-commutative equation, $T_2 \circ T_{13}$, where $\circ$ is the functional composition operator) to generate T_{10}. The three outputs from T_{13} are received with equal probability and transformed by T_2 to produce T_{10}, which inherits the input domain from T_{13} and the output range of T_2. The number of possible unique binary interactions (207) is described by an interaction network (*G*) in the form of a $|T| \times |T|$ matrix; all functional compositions are members of the set of 15 types producing a compositionally closed population of interacting machines. Unsuccessful interactions between machines create the *transitionless* machine T_0, which is prohibited in our model of an interacting community.

automata. This equation assumes that all interactions are possible on each time step, which is consistent with a well-mixed environment with no influx of automata.

Spatial mixing occurred within the population during replication by randomly selecting a lattice site and exchanging the residing automaton with another type positioned on a

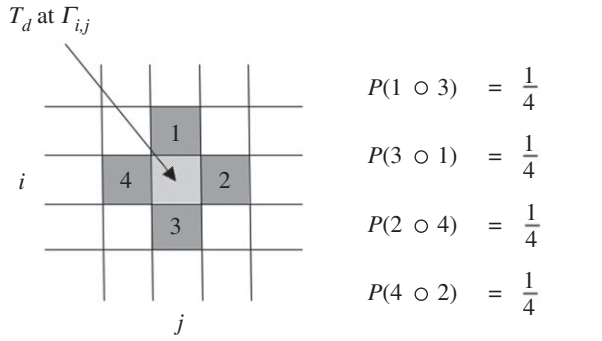

Figure 2. Graphic illustrating the computational model for generating internal production dynamics in a square lattice of *nxn* sites comprising single-state automata of type *T* [17]. The lattice has periodic boundary conditions, i.e. a regular toroid topology, and, as such, an automaton in the top two rows of the lattice can interact with automata directly opposite it in the bottom two rows of the lattice and vice versa. The same condition applies to an automaton on the left edge and right edge of the lattice. Spatial mixing also occurs in the same manner. An automaton (T_d) on lattice site $\Gamma_{i,j}$ is chosen at random for replacement by functional composition involving types (T_a,T_b) selected from the sites (1,2,3,4) adjacent to T_d. Only one pair of neighbours from the two possible pairwise combinations (1,3 or 2,4) is selected to interact according to the non-commutative equation $T_b \circ T_a$, where the order of the interacting pair is selected randomly according to an equal probability of 1/4. If the functional composition generates a new automaton (T_c), this replaces T_d at lattice position $\Gamma_{i,j}$, which is subsequently removed from the population. If no interaction occurs, then a transitionless machine T_0 is generated such that T_d is not replaced and remains on the lattice site. The new population is then subjected to different levels of spatial mixing.

different lattice site along one of the cardinal directions at a distance d selected from a one-dimensional Gaussian distribution with variance v and mean = 0 and rounding d to the nearest corresponding lattice site. This was repeated for c numbers of different sites per production time step. The combination of c and v approximated diffusion within the replicating population such that when $c \to N$ and $v \to n$ the population was well mixed, while for $c \to 0$ and $v \to 0$ the population of automaton had very low mobility [17]. To simulate the coupling of the replicating population to changes in an external environment, randomly generated automaton types replace randomly selected automata in the population at time t with a probability given by Φ, where $0 \leq \Phi \leq 1$. With $\Phi = 0$, no random replacement occurred and population dynamics were driven entirely by the composition of existing automata. We refer to the process of random replacement as influx to convey the notion of the movement of externally generated automata into the population. In contrast, with $\Phi = 1$, the population dynamics were determined entirely by randomly generated automata entering the lattice from the external environment [14]. Twenty-five combinations of the spatial mixing (c, v) and influx dynamics (Φ) parameters were used to simulate a range of fixed environmental conditions to assess the impact on the production dynamics of the automaton population and the emergence of the information niches.

We investigated the effect of intermittent changes in the environmental parameters on the robustness and transition pathways of the information niches to map the fitness landscape. For this, the following modifications in environmental conditions were imposed once a steady-state niche was attained: (i) inversion of the spatial mixing parameter such

that conditions contrary to those in which the niche was produced are imposed, e.g. if a niche was formed in a well-mixed environment then the environmental conditions were reset to simulate a highly restricted movement of the automata (c, $v = 0$); (ii) inversion of the influx setting of new machines into the lattice, e.g. if a niche was produced in the absence of any influx of automata ($\Phi = 0$) then this parameter was reset to $0 < \Phi \leq 1$; (iii) simultaneous perturbations associated with modifications (i) and (ii); (iv) introduction of a type-restricted influx (Φ') of automata that were randomly selected from the specified subset of automaton types (T_6,T_7,T_9,T_{11},T_{13},T_{14}); and (v) simultaneous perturbations associated with modifications (i) and (iv). Perturbations on the initially produced steady-state niche were undertaken for a minimum of 1×10^6 iterations, which was usually sufficient for the population to reconfigure into a new steady-state conformation. The perturbations were then removed by resetting the environmental parameters back to their original values, and changes to the population structure recorded. Consequently, the original (*primary*) niche was re-created or a new (*secondary*) niche was established by perturbing the primary niche.

2.2 Structure and dynamics of information niches

2.2.1. Quantifying niche structure, diversity and the minimum information required for niche generation

The distribution of automaton types in a given population was structurally defined, and was responsible for the range of possible interactions. Changes in population structure, and the consequent diversity of interactions available, was quantified at each time step using the interaction network complexity ($C_\mu(G)$), which measured the amount of information required to describe the probability that each interaction could occur in the population contingent on the current structure of the population [14],

$$C_\mu(G) = -\sum_{f_a f_b f_c > 0} \frac{v^c_{ab}}{V} \log_2 \frac{v^c_{ab}}{V}, \tag{2.2}$$

where

$$v^c_{ab} = \begin{cases} f_a f_b, & \text{if } T_c = T_b \circ T_a \text{ has occurred} \\ 0, & \text{otherwise,} \end{cases}$$

$V = \Sigma v^c$ is a normalizing factor and f_a, f_b are the proportion of automaton types a and b in the population, respectively. Equation (2.2) determines the likelihood of an interaction occurring to produce T_c from the concentration of automata exhibiting the required functional composition. As the population evolves, some automaton types became extinct while others became more populous. As a consequence, automata produced by types that were increasing in concentration were more likely to be produced than those that were dependent on types that had become extinct. Such dynamics were reflected in the complexity of the interaction network, which reduced when some automaton types became extinct. Given that only one new automaton was produced at each time step, every interaction that occurred was *competing* with all other potential interactions. Subsequently, the probability of a specific interaction occurring was contrasted against the sum of the probability of all other possible interactions, as given by the normalization term V. The probability of an interaction occurring to generate an automaton was the sum of the normalized frequencies of those automata responsible for its production. This normalized probability was calculated for each machine type in the population to yield a probability distribution. The information entropy of this probability distribution then yielded the interaction network complexity $C_\mu(G)$. As such, calculating $C_\mu(G)$ provided a signature of the structure of the population at a given moment in time, and, when compared with the initial unstructured compositionally homogeneous population at the start of a simulation, provided a quantitative measure of the reduction in information entropy (or, conversely, the amount of order that was being created within the population) as the network system evolved into a niche.

Quantifying the minimum information required for niche generation was undertaken by defining the production threshold as a measure of the information required to describe the minimum number and type of automata that were required to be produced to create a niche. The production threshold for a niche was determined by calculating the Shannon entropy (H) of the frequency distribution (X) of each automaton type that would need to be produced within a given population,

$$H(X) = -\sum_{i=1}^{|T|} x_i \log_2 x_i, \tag{2.3}$$

where x_i is the proportion of interactions in the population that produce automaton type i and T is the set of all automaton types. The production threshold differed between niches depending on the number of constituent automata, with lower values for those niches in which not all automaton types were present. We used this measure to compare the information required to transition between niches, elucidate how the niches transitioned in response to perturbations in environmental conditions and explain why some niches were more robust than others. In general, the production threshold and interaction network complexity were complementary. The former quantified the information required to generate a niche, whereas the latter quantified the information required to describe a niche after it had evolved to a steady-state distribution, and any interactions that remained between the automata.

2.2.2. Identifying strongly connected production networks

Even in a relatively simple population of interacting entities the number of possible networks that describe all possible sequences of interactions can be significant. Identifying and examining all such sub-networks within a given population was used to identify specific networks responsible for self-organization of the population into a niche. One of the drivers of self-organizing behaviour was nonlinearity caused by positive feedback loops in the system [18], and this was manifested in an interaction network as a strongly connected cyclic topology [19,20]. We developed an algorithm to identify and categorize any sub-network structures in the interaction network (G) that had the motif of a *strongly connected network*, i.e. whereby a subset of automata mutually produce each other:

begin
  W : The set of all possible combinations of sub-networks
  for each w in W
    create adjacency matrix A for w where A_i *are outgoing edges and* A_j *are incoming edges*
      if $SUM(A_i) \geq 2$ AND $SUM(A_j) \geq 2$ *for* EACH *node in w*
        then add w to S
end

This is an exhaustive algorithm that examines all possible combinations (W) of automaton interactions partitioned into many sub-networks (w) ranging in size from two to 15 automaton types. An adjacency matrix (A) was generated for each sub-network to describe the associated topology as a directed graph [21] with nodes and directed edges indicative of an individual automaton type and which automata interact to produce other automaton types, respectively. The adjacency matrix of each sub-network was tested for the characteristic of mutual production between members (i.e. a cycle), whereby each automaton (node) in the sub-network must have: (i) a minimum in-degree of two edges, implying that it is produced by at least one interaction of automata in the sub-network apart from with itself (self-replication), and (ii) a minimum out-degree of two edges, implying that the automaton produces one other automaton apart from itself within the sub-network. A sub-network was considered to be a candidate for a strongly connected network only if all constituent automata fulfil these criteria. The set of candidate strongly connected networks (S) was then examined for dynamic stability.

2.2.3. Determining dynamically stable networks

To identify dynamically stable networks we numerically solved $\mathrm{d}f/\mathrm{d}t = 0$ of equation (2.1) for each strongly connected network (S) identified in the interaction network (G). All sub-networks in S were examined for dynamic stability and the automaton types in the numerical simulation were restricted to those present in the sub-network under consideration. Networks whose production dynamics resulted in extinction of any of the constituent members, or which created new information processors that were not original members of the network, were deemed unstable.

3. Results

3.1. Emergence and properties of primary information niches under fixed environmental conditions

Twenty-five environments were simulated by setting unique combinations of the spatial mixing (c, v) and influx dynamics (Φ) parameters in the range of $0 \leq c \leq N$, $0 \leq v \leq n$ and $0 \leq \Phi \leq 1$ for an evolving population of 90 000 interacting automata distributed equally across 15 different types. The emergence of steady-state network configurations (information niches) under fixed environmental conditions typically required between 1×10^6 and 1×10^7 iterations. After every iteration, the changes in frequency (f) of each automaton type were determined until steady-state conditions were attained. Significantly, six distinct primary information niches (A–F) comprising strongly connected components of self-producing communication channel networks were obtained (figure 3).

3.1.1. Influence of spatial mixing and non-diffusivity

Niche A consisted of a steady-state network of nine automata that emerged from a well-mixed population ($1 \leq c \leq N$, $1 \leq v \leq n$) in the absence of an influx of randomly generated automata ($\Phi = 0$). Six automata became extinct (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) and the remaining nine types differentiated into three distinct clusters exhibiting no growth (T_1, T_2, T_4, T_8), slow growth (T_3, T_5, T_{10}, T_{12}) and fast growth (T_{15}), all of which reached steady-state frequencies after $t = 4 \times 10^5$ time steps (figure 3*a*). T_{15} was produced from 35 interactions and was therefore the most frequently produced automaton. In comparison, automaton types in the slow and no growth clusters were generated from 21 or 15 interactions, respectively, while those that became extinct were produced from only eight interactions involving the (T_7, T_{11}, T_{13}, T_{14}) (six interactions) and (T_6, T_9) (two interactions) sub-groups. Interestingly, extinction of the six automata resulted in a drastic reduction in the number of interactions in the population from 207 to 63 interactions, which were then responsible for producing each of the remaining automata at an equal rate (seven interactions per automaton) and establishing steady-state conditions within the population.

In contrast, simulations of the population production dynamics under fixed conditions of no spatial mixing ($c = 0$, $v = 0$) and no randomly generated influx ($\Phi = 0$) produced niche B, which comprised a four-automaton steady-state network consisting of types T_1, T_2, T_4, and T_8 (figure 3*b*). The population dynamics initially mirrored those observed for a well-mixed environment (niche A), but then exhibited a major transition at $t = 2 \times 10^5$ after which the initial growth of T_{15} and the (T_3, T_5, T_{10}, T_{12}) group was replaced by a rapid decrease in their frequency such that these automata became extinct after approximately 3×10^6 iterations. As a consequence, the (T_1, T_2, T_4, T_8) group, which exhibited no growth in a well-mixed environment (niche A), differentiated into fast growing and non-growing populations of T_2 and T_4, and T_1 and T_8, respectively, with the (T_2, T_4) pair occupying approximately 85% of the final population of niche B produced in the absence of spatial mixing. Under these conditions, interactions between the automata were spatially restricted such that short-range interactions dominated the population dynamics. As a consequence, two mechanisms were responsible for the fast growth of T_2 and T_4 in niche B: (i) independent interactions between T_2 or T_4 with a range of other automata gave rise to self-replication, or alternatively to production of T_1 and T_8, which subsequently interacted with various other automata to generate T_2 and T_4 and (ii) local concentrations of T_2 and T_4 produced a spatial cluster (defined as a contiguous square area of the lattice consisting of nine T_2 or T_4 automata), which acted as a nucleation domain for protected outgrowth.

3.1.2. Influence of influx dynamics

Having simulated the influence of spatial mixing and non-diffusivity on niche formation, we next investigated the effect of introducing an influx of randomly generated automata into an interacting population of automata under a range of mixing conditions. In the presence of both spatial mixing and significant influx dynamics ($0 \leq c \leq N$, $0 \leq v \leq n$ and $0.25 \leq \Phi \leq 0.9$), the emerging steady-state population (niche C) was structured similarly to niche A except that the (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) group no longer became extinct (figure 3*c*). As a consequence, all 15 automaton types survived to produce a heterogeneous population structure comprising four steady-state clusters consisting of (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) with a decreased frequency, (T_1, T_2, T_4, T_8) with constant frequency, and (T_3, T_5, T_{10}, T_{12}) and T_{15}, which exhibited slow and fast growth, respectively. In contrast, simulations of the population production dynamics under spatial mixing ($0 \leq c \leq N, 0 \leq v \leq n$) and with a very high influx of randomly generated automata ($0.9 < \Phi \leq 1$; niche D) indicated that under these conditions the population dynamics were dominated by the influx

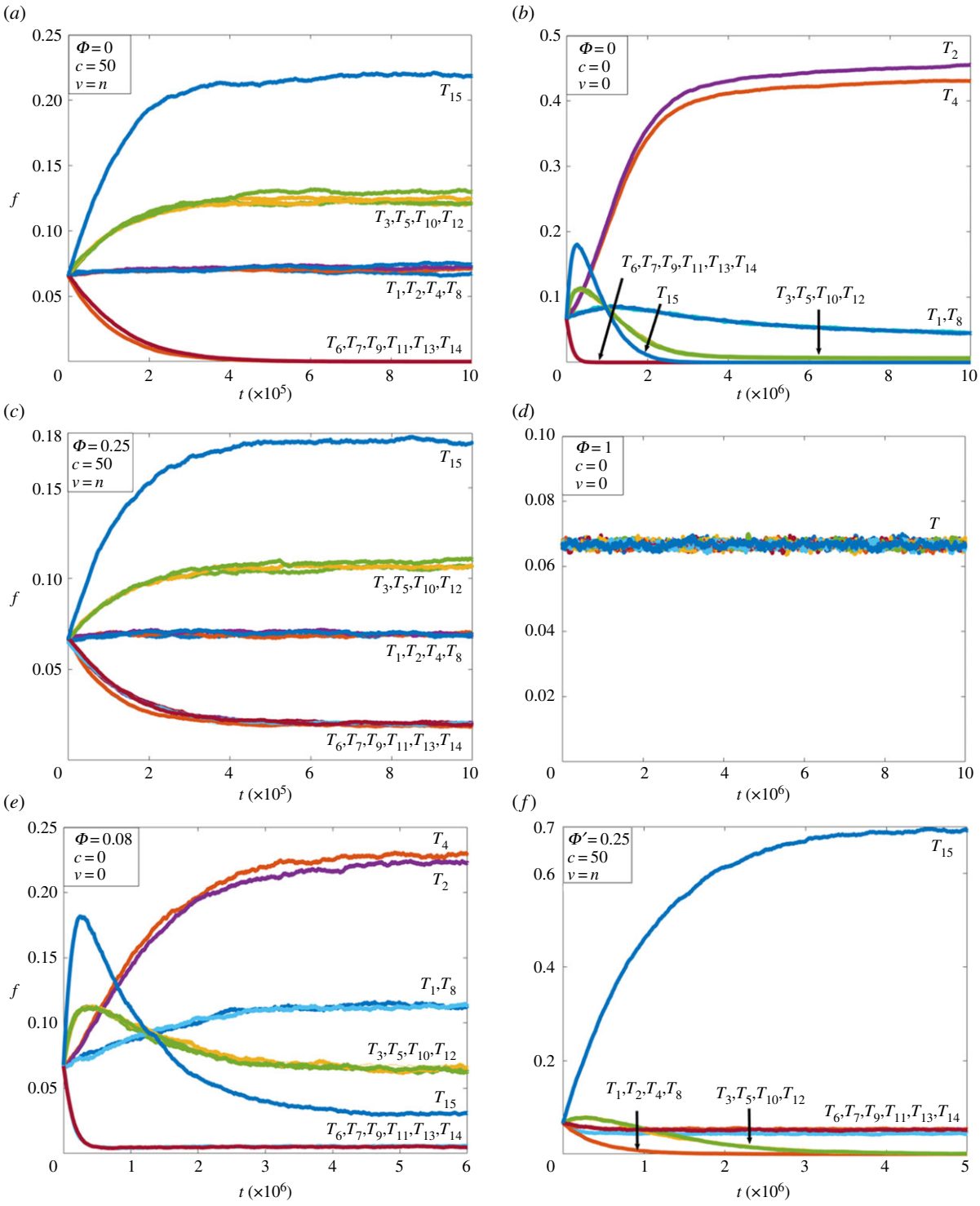

Figure 3. Plots of frequency distributions (*f*) against iteration time step (*t*) for interacting populations of automata under different simulated fixed environmental conditions. The simulations show the evolution of six distinct information niches comprising steady-state networks of selected and clustered information processing channels from an interacting population consisting of 90 000 single-state automata distributed at $t = 0$ equally across 15 different types (shown in different colours) and subjected to three different environment inputs. (*a*) Niche *A*: population production dynamics in an environment with high spatial mixing of automata ($1 \leq c \leq N$, $1 \leq v \leq n$) and with no influx of randomly generated automata ($\Phi = 0$) showing extinction of six automaton types and the emergence of a steady-state distribution of nine survival types arranged into three distinct clusters with one, four or four members after $t = 4 \times 10^5$ time steps. (*b*) Niche *B*: extinction and steady-state survival of 11 and four binary automaton types, respectively, under a highly immobile environment exhibiting no diffusivity ($c = 0$, $v = 0$) and no randomly generated influx ($\Phi = 0$). The survivors are arranged in three sub-groups containing one, one or two members. (*c*) Niche *C*: population production dynamics across a range of mixing conditions ($0 \leq c \leq N$, $0 \leq v \leq n$) and subjected to a considerable rate of influx of randomly generated automata ($0.25 \leq \Phi \leq 0.9$). All automaton types survive to produce a heterogeneous population structure comprising four steady-state clusters consisting of one, four, four and six members. The population is structured similarly to niche *A* except that six members no longer become extinct. (*d*) Niche *D*: under all mixing conditions ($0 \leq c \leq N$, $0 \leq v \leq n$) and with $\Phi > 0.9$ the population dynamics are dominated by the influx of new randomly generated automata from the environment such that the population remains unstructured and compositionally homogeneous over 1×10^5 iterations. (*e*) Niche *E*: with no diffusive mixing on the lattice ($c = 0$, $v = 0$) and with a very low influx rate ($0 < \Phi < 0.1$); the population is structurally similar to niche *B* except that three sub-groups of automaton types ((T_{15}), (T_3,T_5,T_{10},T_{12}) and (T_6,T_7,T_9,T_{11},T_{13},T_{14})) no longer go extinct. (*f*) *Niche F:* with restricted automaton influx ($\Phi' = 0.25$) and under a range of mixing conditions ($0 \leq c \leq N$, $0 \leq v \leq n$) the population evolves to three groups of automata (T_{15}), (T_6,T_7,T_9,T_{11},T_{13},T_{14}) and (T_3,T_5,T_{10},T_{12}), with the group (T_1,T_2,T_4,T_8) going extinct.

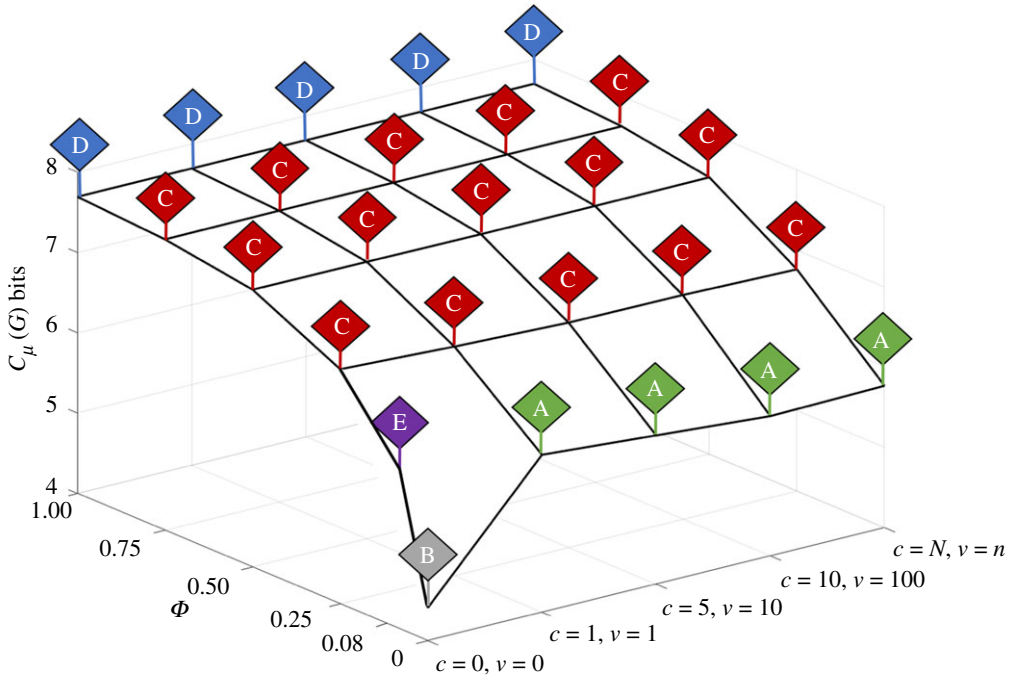

Figure 4. Three-dimensional map of the interaction network complexity $C_\mu(G)$ against environmental parameters (c, v, Φ) showing the information niche landscape. The information niches reside at different levels of $C_\mu(G)$. Note the prevalence of niche *C*. Niche *F*, which is produced under compositionally restricted influx ($\Phi' = 0.25$), is not shown. There is little sensitivity to changes in the interaction network complexity measured for a wide range of values for c and v. In general, spatial mixing has a mild effect on population structure, and given that the interaction network complexity is contingent on structure, results in minor changes to the interaction network complexity.

rate from the environment. As a consequence, the population had no memory of previous interactions, and therefore remained unstructured with a composition uniformly distributed over all 15 automaton types even over 1×10^5 iterations (figure 3*d*). We simulated the population production dynamics under conditions of no diffusive mixing on the lattice ($c = 0$, $v = 0$) and with a very low influx rate ($0 < \Phi < 0.1$). The resulting niche *E* was structurally similar to niche *B* ($c = 0$, $v = 0$; $\Phi = 0$) but showed no automaton extinctions.

Finally, we simulated the population dynamics under a type-restricted influx ($\Phi' = 0.25$) comprising randomly generated automata drawn from a specified subset of automaton types (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}). This specific subset was chosen as it represented the automaton types that were most frequently depleted from the population, or in the case of niches *A* and *B* became extinct. Thus, by restricting the environmental influx to this subset, we not only increased their concentration in the environment but also increased the probability that an automaton type from this subset would be re-introduced into the population during the simulation. As a consequence, rapid decay and extinction of (T_1, T_2, T_4, T_8), slow decay and extinction of (T_3, T_5, T_{10}, T_{12}) and rapid growth of T_{15} were observed to produce niche *F*. Niche *F* was structured into two groups consisting of a dominant automaton (T_{15}) that occupied 70% of the population, along with a constant concentration of the (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) cluster, which was sustained by the limited influx dynamics into the lattice. Significantly, T_{15} exhibited rapid growth because it was the only automaton produced (via eight interactions) by the restricted subset of influx automata (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}), and was the only self-replicator in the population.

3.1.3. Niche landscape and niche construction

Niche *C* was predominant across a wide range of fixed conditions of spatial mixing and random influx, indicating that the network constellation producing the distinctive four clusters was extremely robust. In contrast, niches *A* and *D* were produced under a limited set of conditions ($1 \leq c \leq N$, $1 \leq v \leq n$; $\Phi = 0$ and $0 \leq c \leq N$, $0 \leq v \leq n$; $\Phi > 0.9$, respectively), and *B* represented a singularity at $c = 0$, $v = 0$; $\Phi = 0$. The corresponding information landscape was mapped by plotting the interaction network complexity values ($C_\mu(G)$) for niches produced under different environmental conditions (figure 4).

A niche with a higher interaction network complexity has more interactions and a more uniform distribution of automata and hence there is more uncertainty over what the next automaton to be produced will be. By contrast, there is less uncertainty in a lower complexity niche for the opposite reasons, i.e. fewer possible interactions and a non-uniform population and therefore more certainty over which automata are likely to be produced. An alternative interpretation is that more complex niches host a greater degree of competition between automata to reproduce due to each automaton having a lower probability of being produced than an automaton in a less complex niche (as measured by a lower interaction network complexity).

The initially unstructured and uniformly distributed population at $t = 0$ had a $C_\mu(G)$ value of 7.7 bits that represented all 207 possible interactions, and this reduced to 5.8 bits for niche *A* (63 interactions) and to 2.6 bits for niche *B* (eight interactions), indicative of higher levels of structuration particularly for niche *B*. In contrast, the $C_\mu(G)$ value for niche *C* was 7.0 bits, which represented all 207 interactions and a small decrease in complexity (−0.7 bits) due to structuring of the population into four clusters. As niche *D* contained no changes in the frequency distribution of the original population, the $C_\mu(G)$ value remained at 7.7 bits. Niche *E*, which had a similar spatial lattice structure to niche *B* but with inclusion of all automaton types in the population, had a $C_\mu(G)$ value of 6 bits. This represented all 207 possible

interactions but with more and less structure than niche *C* and niche *B*, respectively. In general, the rates of formation of the information niches were decreased as the rate of spatial mixing decreased and/or the influx rate of new randomly generated automata increased. For example, growth of the (T_2, T_4) group in niche *B* was reduced as $0 < \Phi \leq 0.1$ and disappeared with $0.1 < \Phi \leq 1$. This indicated that increasing the number of automaton types persisting in the population due to a continuous influx from the environment ($\Phi > 0$) destabilized the onset of structuration and the concomitant emergence of steady-state networks. In contrast, at $\Phi = 0$, 11 automaton types became extinct in niche *B*, which reduces the robustness of the network with respect to its ability to self-generate.

We executed an algorithm to identify interaction networks in a one-state automaton population that had strongly connected topologies characteristic of mutual production. The algorithm generated 7831 interaction networks ranging in size from two to 15 automata and exhibiting different levels of specialism (figure 5*a–d*). A subset of 129 networks was identified as strongly connected, implying that they were closed under composition. Of these, 29 were dynamically stable, i.e. under dynamical conditions each automaton in the network continued to be produced at a rate that no single automaton was over-produced (leading to complete dominance) or under-produced (leading to decay and ultimately extinction) within the population.

Such networks are similar to meta-machines [16], and endured indefinitely unless subjected to changes in the environmental conditions that disrupted the population dynamics. Of the 29 closed and stable networks, niche *A* (high spatial mixing ($1 \leq c \leq N$, $1 \leq v \leq n$) and no intake dynamics ($\Phi = 0$)) contained 28 (the closed and stable network $\{T_6, T_9\}$ became extinct with time), while niche *B* with no lattice diffusion and no random influx ($c = 0$, $v = 0$; $\Phi = 0$) contained only one. In contrast, niche *C*, which emerged under a wide range of population mixing and influx conditions ($0 \leq c \leq N$, $0 \leq v \leq n$; $0.25 \leq \Phi \leq 0.9$), contained all 29 dynamically stable strongly connected networks. As expected, niche *D* produced under high levels of spatial mixing ($0 \leq c \leq N$, $0 \leq v \leq n$) and very high influx ($\Phi > 0.9$) did not contain any stable networks.

We also searched for stable networks of production that were not only closed under composition but also irreducible. Production networks were irreducible if removal of one automaton resulted in dynamic instability that led to the decay of the network to a single automaton. Of the 29 dynamically stable networks, a subset of 12 networks termed *elementary networks* was identified as being closed, stable and irreducible (figure 5*e*). Niches *A*, *B*, *C* and *D* contained 11, 1, 12 and 0 elementary networks and niches *E* and *F* contained 12 and 0 elementary networks, respectively. Significantly, there was an association between niches with a higher number of elementary networks and their persistence across a range of environmental conditions, e.g. niches *A* and *C* collectively occupied approximately 75% of the information landscape (figure 4). While this was not a universal finding—niche *E* occurred only once and this was due to its formation exclusively in a low influx and low diffusive environment—it did suggest a degree of robustness conferred on a niche courtesy of the presence of more than one elementary network.

The presence of the elementary network $\{T_6,T_9\}$ in niche *C* was a direct consequence of the influx of randomly generated automata from the environment as this elementary network did not persist in the absence of any influx (niche *A*). Significantly, information niche *A* was constructed from a hierarchical organization in which the successive combination of elementary networks (level 0) produced intermediate networks (level 1), which in turn were integrated and embedded in a higher-order structure (level 2) (figure 5*f*). There were 15 construction pathways by which the higher-order network produced niche *A*, with each pathway the result of a unique combination of elementary and intermediate networks. Each network in the hierarchical organization was closed and dynamically stable. In contrast, niche *B* with a single elementary network was non-hierarchical.

The pathway to niche *C* involved the same elementary networks as niche *A*, except that in the presence of an influx of randomly generated automata ($0 < \Phi \leq 0.9$) the group (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) became organized into strongly connected networks that were dynamically unstable, and were therefore not part of the network hierarchy. Significantly, niches *A* and *C* consisted of automata that were each produced by at least two elementary networks, indicating a level of redundancy in the organization (figure 5*f*); for example, deconstruction of niche *A* indicated that the redundancy at level 1 involved decomposition of the intermediate networks into a subset of six ($\{T_1, T_3\}$, $\{T_1, T_5\}$, $\{T_3, T_{12}\}$, $\{T_5, T_{10}\}$, $\{T_8, T_{10}\}$, $\{T_8, T_{12}\}$) of the total of 12 elementary networks.

3.2. Dynamics of information niches under environmental perturbations

To investigate the influence of environmental perturbations on the robustness and possible transitions of the primary information niches we simulated the response in the population dynamics to intermittent changes in the parameters *c*, *v*, Φ and Φ' (figure 6). These parameters were varied to simulate five types of perturbation that were imposed on each primary niche (niches *A–F*): (i) switching of lattice diffusivity to a value opposite to that initially associated with niche formation; (ii) switching of the influx rate to one of four possible values ($\Phi = 0$, $0 < \Phi < 0.1$, $0.1 \leq \Phi \leq 0.9$ and $0.9 < \Phi \leq 1$), which in each case corresponded to a parameter opposite to that initially associated with niche formation; (iii) application of (i) and (ii) concurrently; (iv) restricting the influx composition from a random selection of 15 automaton types to a confined group of six specified automata (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) at a rate $\Phi' = 0.25$; and (v) application of (i) and (iv) concurrently. In general, the results indicated that imposing environmental perturbations on the primary niches produces transformations in the internal structure of the population through the growth or decay in various automaton types, which under certain conditions (introducing diffusive mixing into niche *B*/*E* or removing influx into niche *F*) generated two new secondary niches (niche *X* and niche *Y*). We then perturbed these secondary niches by resetting the environmental parameters to those initially used for the formation of the associated primary niche to assess the reversibility of the niche transitions across the information landscape (figure 6*c–d*).

In total, 39 transitions between six primary niches and two secondary niches were identified (figure 6*e*). In some cases, the transitions were unidirectional. For example, niches *A* and *C* were established after 7.5×10^5 iterations under well-mixed conditions with no or low intake dynamics ($c = N$, $v = n$; $\Phi = 0$ or $c = N$, $v = n$; $\Phi = 0.08$), respectively, and then

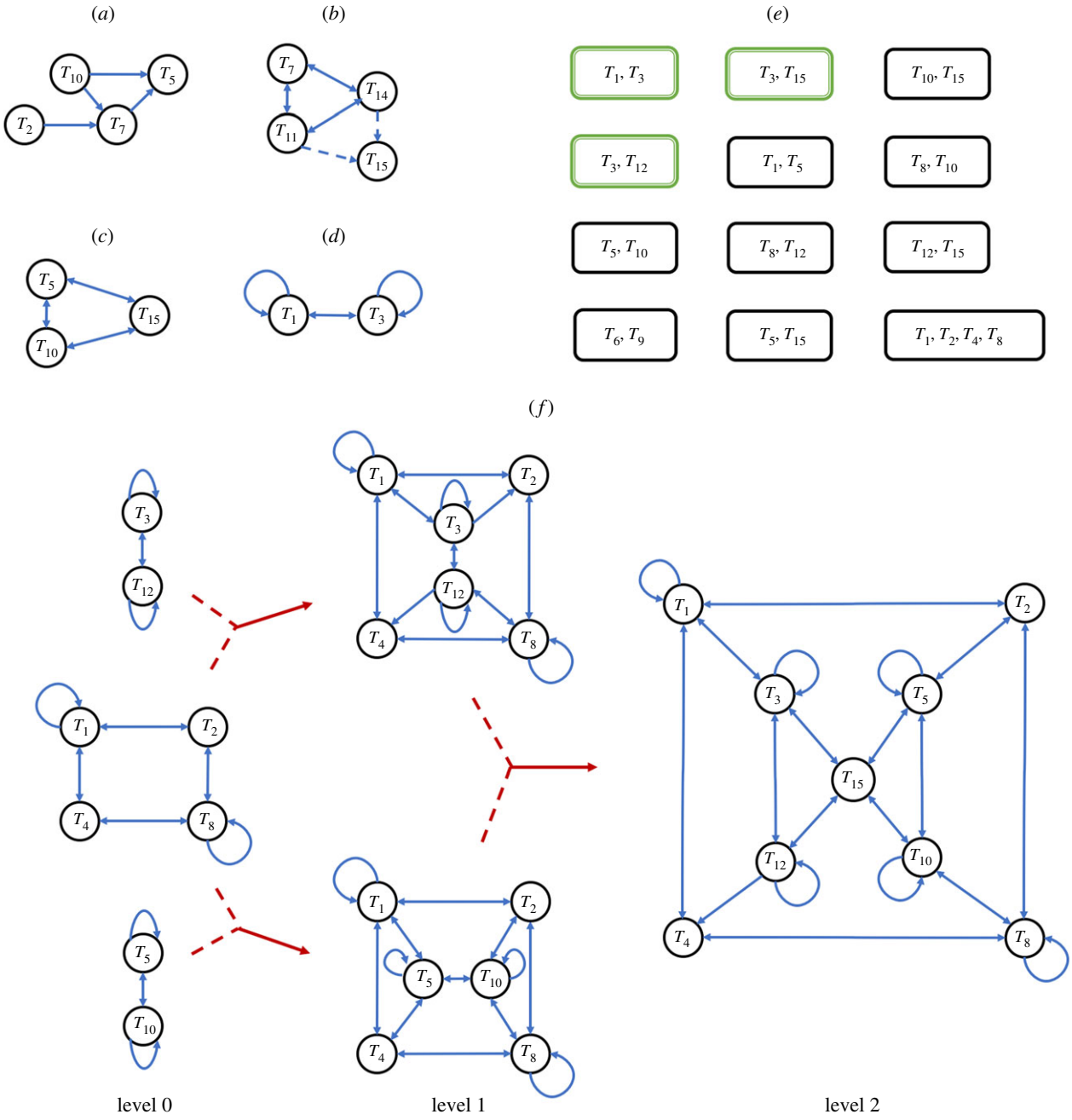

Figure 5. (*a–d*) Examples of the different types of network topologies generated from all combinations of interactions between automata in order of increasing specialism. (*a*) The most general topology (7702 identified types). The topology consists of a directed network in which each node represents an automaton and edges (arrows) signify that the automaton is involved in the production of the automaton positioned at the termination of the edge. For example, automata T_2 and T_{10} interact to produce T_7, which interacts with T_{10} to produce T_5. In this example, the algorithm identifies the three networks $\{T_2, T_7, T_{10}\}$, $\{T_5, T_7, T_{10}\}$ and $\{T_2, T_5, T_7, T_{10}\}$. (*b*) Network with *apparent* strongly connected components (100 identified types), indicating that the constituent automata mutually produce each other; however, over time automata are also produced outside of the network (dashed arrows leading from T_{11} and T_{14}), or the system becomes dynamically unstable because of competition within the same network that leads to extinction of one or more of its members. Edges with double arrows indicate that the connected automata are involved in producing each other. (*c*) Example of a strongly connected network (17 identified types) that only produces automata within the network, is dynamically stable and can be reduced into smaller sub-networks. (*d*) Example of a strongly connected network (12 identified types) that is dynamically stable and irreducible (elementary networks). A curved arrow indicates that the automaton is involved in its own production. (*e*) All 12 elementary networks of a one-state automaton population. Some automata are produced by more than one network and this is highlighted for T_3 (green boxes). Multiple pathways to producing the same automaton (redundancy) confers a degree of robustness to the continued production of an automation even if an elementary network decays due to the extinction of one of its constituents. By comparison, T_6 and T_9 are only produced by one elementary network and these automata often become extinct. Niche *A* consists of all elementary networks except $\{T_6, T_9\}$; niche *B* consists of only one network $\{T_1, T_2, T_4, T_8\}$; and niche *C* consists of all of the elementary networks. (*f*) An example of a pathway to the bottom-up hierarchical construction of niche *A* based on the integration of three elementary networks (level 0) that combine to form two larger networks (level 1), which become embedded at level 2. Note that T_{15} is only produced when the level 1 networks are combined. Double arrows indicate that the associated automata are involved in producing each other and curved arrows indicate an automaton that is involved in self-production.

subjected to an extreme perturbation by switching the lattice diffusivity to zero ($c = 0$, $v = 0$). As a consequence, over 1.25×10^6 iterations niches *B* and *E* emerged in each population, respectively, with T_{15} experiencing a rapid decay while T_2, T_4 underwent fast growth. Once niches *B* or *E* were fully established, we re-adjusted the parameters to their original

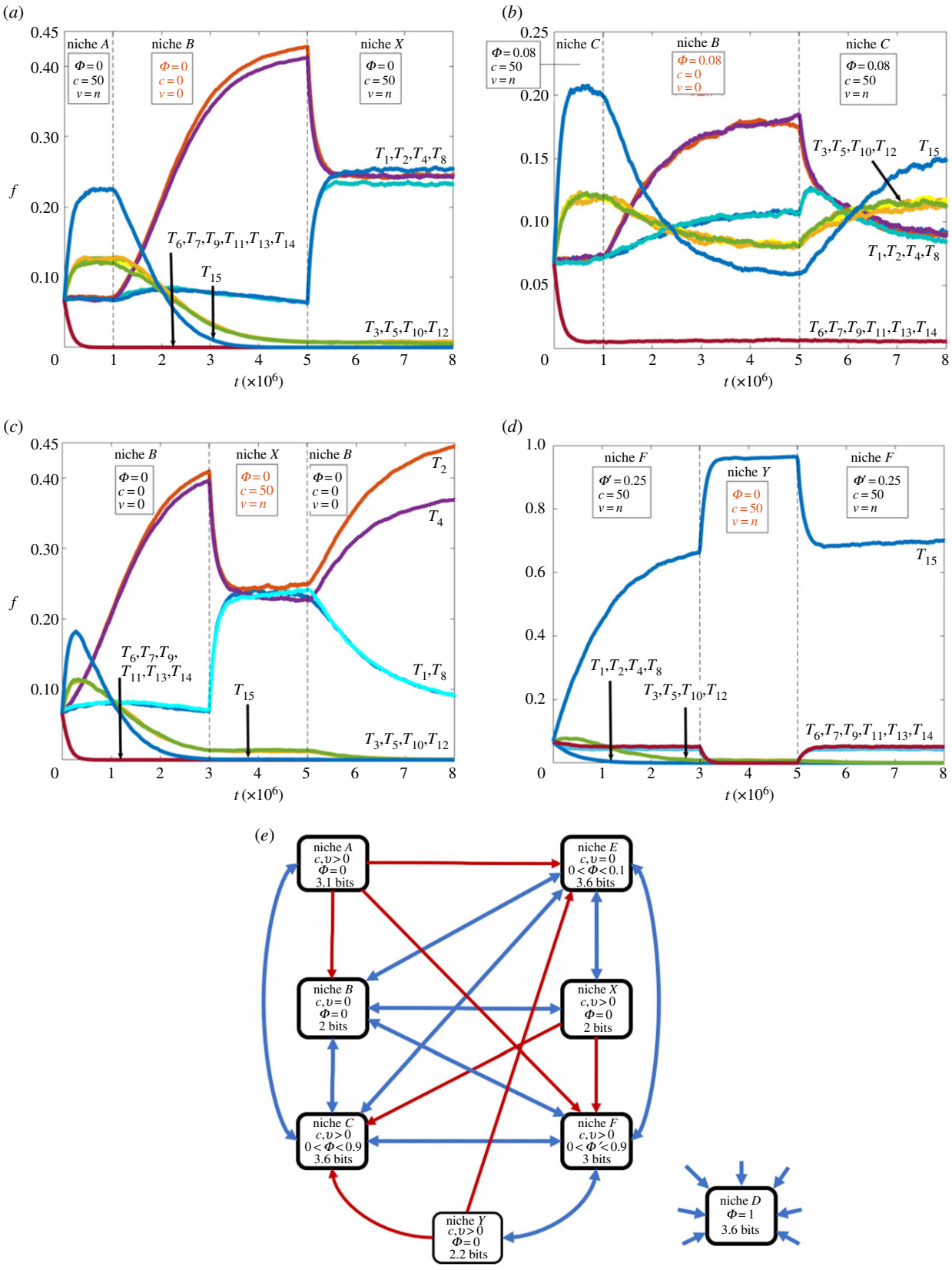

Figure 6. Plots of frequency distributions (f) against iteration time step (t) showing the population dynamics when subjected to intermittent and extreme changes in environmental conditions (red text). (*a*) Primary information niche *A* was established after 1×10^6 iterations, and then the lattice diffusivity reduced to zero. Niche *B* emerged within 5×10^6 iterations and subsequently resetting the parameters to their original values formed a new secondary niche *X*, which was distinguished by two groups of automata (T_1,T_2, T_4, T_8) and (T_3, T_5, T_{10}, T_{12}). (*b*) Similarly, primary niche *C* was established after 1×10^6 iterations and then the lattice diffusivity reduced to zero leading to the reversible emergence of niche *E* after 5×10^6 iterations; resetting the parameters to their original values re-created niche *C*. (*c*) Formation of the secondary niche *X*; niche *B* formed after 3×10^6 iterations and then the lattice diffusivity was increased for 2×10^6 iterations to generate niche *X* after which the perturbation was removed and the population transitioned back to niche *B*. (*d*) Primary niche *F* was established under type-restricted automaton influx ($\Phi' = 0.25$), and then the population perturbed by removing the intake restriction to produce the homogenized secondary niche *Y* comprising the self-replicator T_{15}; resetting the parameters led to the reverse transition back to niche *F*. (*e*) Information niche transition diagram; each box represents a niche and the associated environmental parameters indicate the conditions under which the information niche forms, and the production threshold of the niche in binary digits. Arrows between niches indicate possible transitions and whether they are irreversible (red single arrows) or reversible (blue double arrows). Niche *D* is a special case as it represents an unstructured, uniformly distributed population, which can be produced from perturbing all primary and secondary niches by setting $\Phi = 1$.

values, and assessed how the emerging populations responded. Niche C was re-established within 1×10^6 iterations, indicating that the C to E transition was reversible across the information landscape under the imposed environmental conditions, while niche A was not re-established from niche B. Instead, niche B transitioned into a new niche (niche X), which consisted of eight automaton types clustered into two groups (T_1, T_2, T_4, T_8) and (T_3, T_5, T_{10}, T_{12}) (figure 6*a*,*b*). Secondary niche X was also produced from niche E by introducing lattice diffusivity into the simulations. Increasing the number of long-range interactions within the highly structured populations of niches B and E eliminated the T_2 and T_4 domains such that the production dynamics were dominated by the elementary network $\{T_1, T_2, T_4, T_8\}$, which produced each of its members with equal probability. This led to a transient period with a reduction in the number of T_2 and T_4 automata and corresponding increase in the number of T_1 and T_8 automata until a new steady state was reached after approximately 5×10^5 iterations (figure 6*c*).

Secondary niche Y was generated by perturbation of primary niche F, which was produced under restricted influx conditions ($\Phi' = 0.25$) via switching off the partial influx of new automata ($\Phi' = 0$) (figure 6*d*). Under the new environmental conditions, the T_{15} frequency, which comprised approximately 70% of the population of niche F, increased rapidly to almost 100% in niche Y to produce a homogenized population. This was principally because (i) T_{15} could be generated from 21 interactions including a high level of self-replication and (ii) the clusters (T_7, T_{11}, T_{13}, T_{14}) and (T_6, T_9) were each produced from only six and two interactions, respectively, and collectively did not form a closed and stable network of production.

The production threshold was calculated for each niche and the loss or gain of information between niches undergoing reversible or non-reversible transitions examined. As shown in figure 6*e*, the production threshold of primary niches C, D and E was 3.6 bits, niche A was 3.1 bits, and niches F and B was 3 bits and 2 bits, respectively. The production thresholds for the secondary niches X and Y were 2 and 2.2 bits, respectively. As the production threshold relates to how much information is required for a niche to persist via the continual production of certain automata, in general transitions within the niche landscape occurred when there was a reduction or no significant change in the information content. However, transitions that resulted in a loss of information and a subsequent reduction in the production threshold of the population were irreversible unless sufficient information was added from the environment. For example, niche A (3.1 bits; $0 < c \leq N$, $0 < v \leq n$; $\Phi = 0$) transitioned to niche B by setting the lattice diffusivity to zero (c, $v = 0$), which resulted in a reduced information content (2 bits) because extinction of T_{15} reduced the number of possible interactions in niche B. Re-setting the parameters to enable lattice diffusivity ($0 < c \leq N$, $0 < v \leq n$; $\Phi = 0$) did not re-establish niche A because increasing spatial mixing did not provide additional information content (T_{15} was irredeemably lost from the population). Instead, niche B transitioned into niche X (2 bits) that had the same information content as niche B but a different steady-state configuration. Indeed, the only way to re-gain lost information was through an influx of automata from outside the population by increasing the Φ parameter. Thus, the transition from niche C ($0 < c \leq N$, $0 < v \leq n$; $0 < \Phi < 0.9$) to B (c, $v = 0$; $\Phi = 0$) was reversible because the initial perturbation step was linked with a reduction of information from 3.6 to 2 bits (figure 6*e*), and the return pathway associated with an increase in new information due to the re-established environmental influx of automata.

Based on the above analysis, the robustness of each niche within the information landscape was observed to be dependent on the environmental conditions under which it was formed, and the nature of any subsequent perturbations. In particular, niches that were generated under zero influx conditions resulted in the extinction of six (T_6, T_7, T_9, T_{11}, T_{13}, T_{14}) of the 15 types of automata, while all the automaton types were retained in niches constructed under high influx conditions. Robust niches such as niches C, D, E and F could recover from any type of perturbation, and were associated with high information environments characterized by the presence of lattice diffusivity ($0 < c \leq N$, $0 < v \leq n$) and some environmental influx ($0 < \Phi < 0.9$). Conversely, niches that were less robust were produced in low information environments characterized by zero diffusivity (c, $v = 0$) and no influx of automata ($\Phi = 0$).

4. Conclusion

We have examined a self-producing system in a pre-evolutionary/pre-genetic scenario by extending the finitary process soup model [14] to investigate the influence of environmental conditions and perturbations on the dynamics and emerging organizational complexity of an interacting population of single-state information processing entities (automata). Our simulations indicate that dynamically stable strongly connected networks of mutually producing automata emerge under specific environmental conditions associated with changes in the degree of spatial lattice mixing and influx dynamics. The emergence of a limited number of these information niches suggests an underlying fitness landscape, which sculpts the self-organizing community of interacting automata into a self-referential system that is contingent on the interplay of internal and external population production dynamics (figure 7). In this perspective, the information niche represents a nexus between four key processes: (i) the mutual production of automata and formation of closed and stable networks, (ii) emergence of a hierarchical interaction network structure, (iii) onset of dynamic stability in the networks of production, and (iv) redundancy within the population and interaction network.

Our simulations indicate that an information niche was more robust and viable with increasing levels of redundancy, as each automaton was produced by at least two different and independent elementary networks, and the associated modularity enables effective niche recovery when subjected to extreme environmental perturbations. Among the fitness landscape, niches C and E are able to reconstruct when subjected to fluctuating environmental parameters principally due to modulating the interface with the environment by coupling of the internal production dynamics to the randomly generated intake of new automata. Significantly, reversible niche transitions are only allowed if accompanied by an equal or increased level of information production. In some cases, the environmental perturbation generates additional information that drives the niche transition, and as such acts as an exogenous source of diversification of the population. Thus, taken together our simulations show that characteristics indicative of mutual production and redundancy confer resilience on the dynamics and emerging organizational complexity of interacting/replicating populations of simple information processing entities.

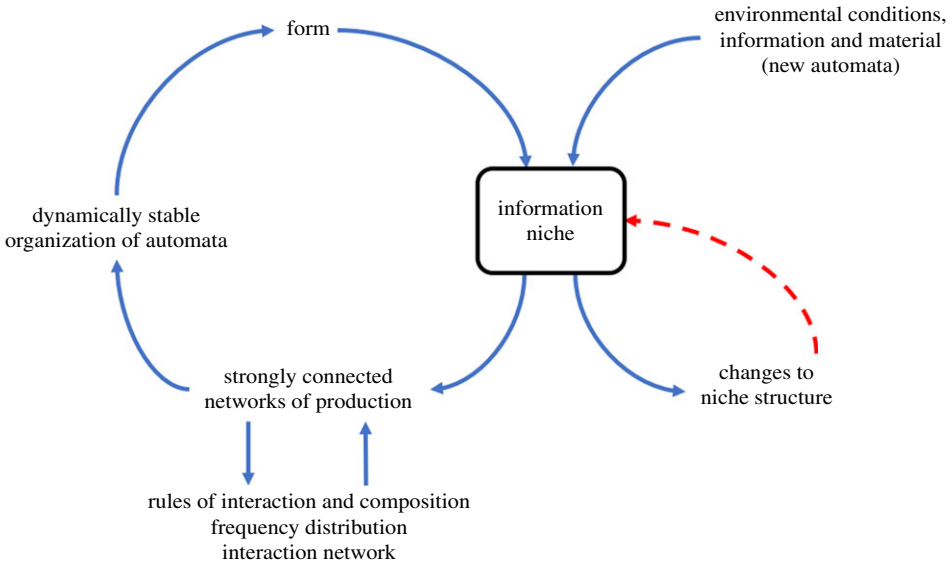

Figure 7. The information niche as a nexus: interactions between automata according to intrinsic (rules of composition and competition) and extrinsic (changes in frequency distribution and interaction network) factors generate strongly connected networks of production that evolve to dynamically stable organizations depending on the coupling with environmental factors (spatial mixing/intake dynamics) to form an information niche. The niche serves as a nexus as it is responsive to external factors such as changes in environmental conditions, information content and input dynamics, as well as to internal changes in structure. The circularity generates a compositionally closed system with the niche acting in a top-down manner to influence the networks of production, thereby maintaining its own identity and demonstrating proto-autopoietic properties.

Within a more general context, our model describes a basic mechanism for coupling environmental parameters into a community of interacting objects that function as communication channels, and therefore offers a new approach for studying the onset of autopoiesis within both a prebiological scenario and bottom-up synthetic biology context. We demonstrate that the emergence of information niches occurs without the introduction of novel forms into an environmental fitness landscape, suggesting that communities of interacting entities such as chemically active synthetic protocells [22,23] could become hierarchically structured and dynamically stable over time even in the absence of evolution. Such observations provide insights into how simple informational transitions between interacting members of a consortium could lead to self-sustaining structured populations comprising proto-autopoietic networks, and could therefore initiate a bridge in the transition from inanimate to living matter via a collective process of protocell self-production operating under non-evolutive/self-replication conditions. Moreover, this in turn might provide a resilient platform for the onset of evolutionary processes responsible, for example, for the emergence of protolife entities from prebiotic inanimate systems. While closed systems based on single causal state automata are incapable of simulating evolution in the Darwinian sense due to the absence of novelty in the automata types produced over successive generations, the functional composition of two-state automata is known to generate communication channels exhibiting entirely novel features [16], suggesting that the environmental dependence of such communities would provide a rich landscape for modelling more complex aspects of autopoiesis. Simulations based on these multi-state systems are the focus of future work.

Data accessibility. The information niche model has been implemented in Matlab and the code and associated files are available online at https://github.com/rjcarte/Information-Niches.

Authors' contributions. R.J.C. implemented and developed enhancements to the finitary process soup model in Matlab, designed and ran all simulations, and performed analysis of the simulation results. S.M. coordinated the study. All authors contributed to the conceptual development of the framework, discussed the simulation results and contributed to the writing of the manuscript. All authors gave final approval for publication.

Competing interests. We have no competing interests.

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CHAPTER 5

RESULTS II - TWO-STATE INFORMATION NICHES

5.1 Introduction

This chapter describes the results from simulating an exclusively two-state automata population. The following simulations were executed:

- Simulation of a two-state automata population self-organising to a niche under well-mixed conditions (see section 5.2)
- Simulation of a two-state automata population self-organising to a niche under low diffusivity conditions (see section 5.3)
- Simulation of a two-state automata population self-organising to a niche under conditions of (i) intermittent and, separately (ii) constant, influx of externally generated automata (see section 5.4)

To verify the results each simulation was repeated five times. All subsequent re-runs accurately re-produced the same outcomes and any differences were minor and due to the stochastic nature of the model. Only one of the results from each simulation is reported here as the differences were deemed inconsequential to the subsequent analysis and interpretation of the results. Box 5.1 has important information on the numbering system used during these simulations to identify individual two-state automata.

Box 5.1 An important note on the referencing of individual automata

Each individual two-state automata in this chapter is referenced sequentially in the range $T_1 ... T_{1873}$. This should not be confused with the notation used to reference the one-state automata ($T_1 ... T_{15}$) e.g. where the $T_1 - T_{15}$ two-state automata are referenced in this chapter these are not the same automata as the one-state automata that are referenced as $T_1 - T_{15}$ in Chapter 4. Chapter 7 - which examines mixed one-state/two-state automata populations - explains the correct referencing of the automata to be used in interpreting the results that are described therein.

5.2 Emergence of a two-state automata niche under well-mixed conditions

The simulation was initialised with a population of 90,000 two-state automata on a 300×300 lattice of 1,873 unique types equating to an average of 48 automata of each type. The simulation was run for 2×10^6 iterations under environmental conditions of diffusive mixing ($c = N, v = n$) and no influx of external automata ($\Phi = 0$). This resulted in a niche (niche $2A$) consisting of 21 automata with all other automaton types going extinct (see Figure 5.1).

The simulation was repeated and produced a near identical result with a steady-state structure with only minor differences due to the stochastic nature of the automata replacement algorithm. However, a third run produced a different niche (niche $2B$) that had the same number of automata (21) as niche $2A$ but now consisted of the automata that had previously competed and decayed in the previous two simulations. Repeated simulation runs indicated that each niche could come to dominate and that this appeared to be probabilistically determined. Analysis of the interaction network revealed that these niches were generated from strongly connected networks whereby the automata constituting niche $2A$ mutually produced each other (and the same was true for the automata in niche $2B$). This insight led to the observation that competition was occurring at two levels: at the individual automata level where pairs of automata were competing with each other e.g. T_{712} from niche $2B$ competes with T_{775} from niche $2A$, T_{55} competes with T_{36}, and so on (see Table 5.1), and (ii) at the network level where collectively the performance of all automata in the two strongly connected networks constituting niche $2A$ and $2B$ had an impact on the individual competitiveness of each of their constituent automata (see Figure 5.2 and Figure 5.3 for the automata in niches $2A$ and $2B$ respectively). Given the

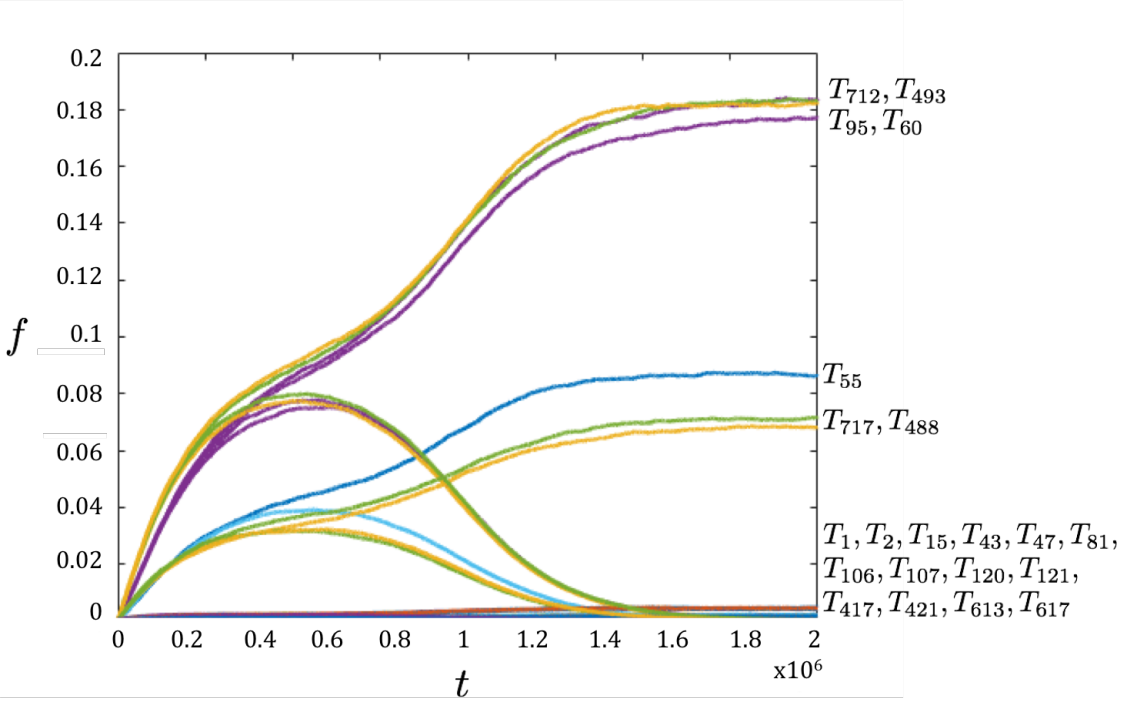


Figure 5.1: Simulation of a two-state population under well-mixed conditions showed an initial stage of competition between two different subsets of automata with one subset eventually dominating whilst the other decayed rapidly. This divergence occurred at the 10^5 iteration. The result was a niche consisting of 21 automata (niche $2A$). Repeated simulations revealed that occasionally the other competing subset of automata came to dominate the population to create a new niche (niche $2B$) with a near identical steady-state structure.

interconnected nature of a niche, all automata in a given niche benefited from one or more of their members out-competing rival automata in the other niche. The likelihood of one niche out-competing the other appeared to be probabilistically close to parity. The stochastic nature of how automata were chosen for interaction and therefore which automata were produced was determined as the reason for the alternating dominance between the two niches over repeated simulation runs.

Compared to the one-state population (see Chapter 4) these results indicated that in a population with a higher average structural complexity[1] three levels of competition had occurred: (i) between individual automata; (ii) between networks of automata; and (ii) between niches. As can be seen in Figures 5.2 and 5.3, the constituent automata in niches $2A$ and $2B$ were topographically identical and the information they processed was the mirror image of the other niche. Each niche processed the exact same information: 20 transitions of $0 \mid 0$, 20 transitions of $0 \mid 1$, 20 transitions of $1 \mid 0$ and 20 transitions of

[1]All one-state automata have $C_\mu(T) = 0$ bits compared to an average of $C_\mu(T) = 0.94$ bits in the two-state population.

category	niche $2A$	f	niche $2B$	no. edges	no. productions
Fast Growth	T_{95}	0.21	T_{102}	1,884	11,700
	T_{60}	0.2	T_{39}	1,884	11,700
	T_{493}	0.18	T_{411}	1,874	22,805
	T_{712}	0.17	T_{775}	1,522	22,805
Medium Growth	T_{488}	0.09	T_{402}	1,795	9,519
	T_{717}	0.09	T_{766}	1,874	22,805
	T_{55}	0.058	T_{36}	1,522	5,980
Slow Growth	T_{15}	0.0007	T_{40}	1,411	1,595
	T_{107}	0.0006	T_{137}	1,401	1,088
	T_{2}	0.0006	T_{4}	1,411	1,595
Slow Decay	T_{47}	0.0004	T_{22}	1,411	1,595
	T_{81}	0.0004	T_{79}	1,411	1,595
	T_{106}	0.0003	T_{561}	1,322	758
	T_{617}	0.0003	T_{134}	1,322	758
	T_{120}	0.0003	T_{204}	1,401	1,088
	T_{417}	0.0003	T_{303}	1,322	758
	T_{421}	0.0003	T_{309}	1,401	1,088
	T_{613}	0.0002	T_{555}	1,401	1,088
	T_{121}	0.0002	T_{207}	1,322	758
	T_{1}	0.0002	T_{3}	1,510	1,223
	T_{43}	0.0001	T_{20}	1,510	1,223

Table 5.1: The competing niches in a two-state population consisted of symmetrical automata e.g. the automata T_1 in niche 2A with the transitions $\{0 \mid 1, 0 \mid 0\}$ had a symmetrical twin T_2 in niche 2B with the transitions $\{1 \mid 0, 0 \mid 0\}$ however they did not interact to produce other two-state automata. Under well-mixed conditions these competing pairs contributed to, and benefited from, the replicative performance of the automata that also constituted their respective niches. The automata from each niche were categorised (e.g. Fast Growth) according to the rate at which they were produced with respect to their initial f which was 0.0005 for each automaton. The f values shown in this table correspond to each niche e.g. automata type T_{95} constituted 21% (0.21) of the population in niche $2A$ and, similarly, its symmetrical twin automata type T_{102} constituted 21% of the population of niche $2B$.

$1 \mid 1$. However, individual automata were processing information differently from their counterpart automata in the other niche. Furthermore, as the population evolved the large majority of automata went extinct and the remaining automata were produced the same number of times (15) which led to the steady-state structure that defined the niche.

The two-state interaction network consisted of 1,873 vertices and 355,484 edges representing the number of potential interactions that produced two-state automata. Of those potential interactions 220,476 produced the 42 automata that constituted the two niches $2A$ and $2B$. For each niche there were 110,238 interactions that produced the automata within that niche with 61.86% (68,189 interactions) producing the High Growth automata, 34.23% (37,737 interactions) producing the Medium Growth automata and 3.91% (4,312

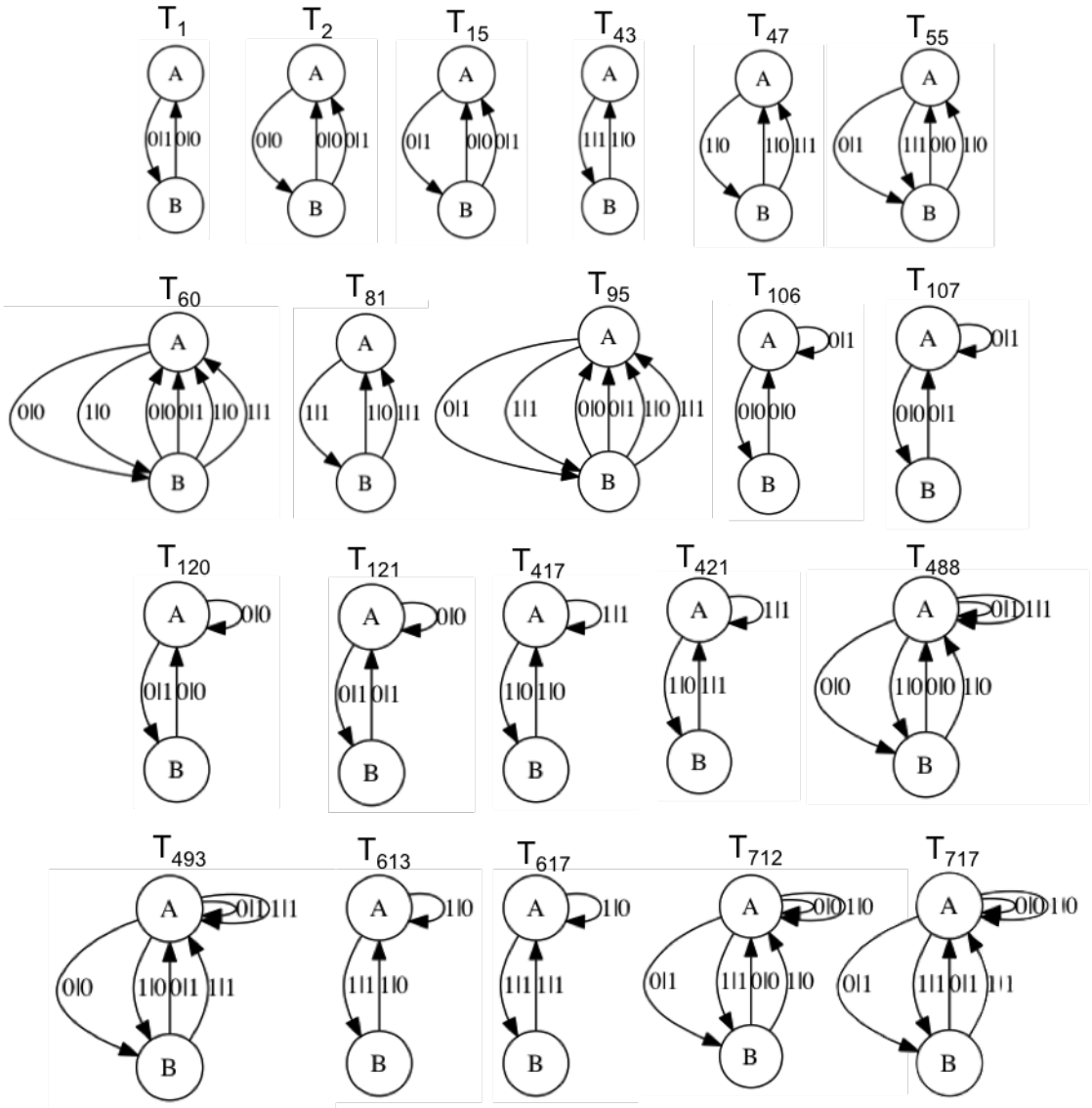


Figure 5.2: The 21 two-state automaton types that constituted niche 2*A*. Taken from [121].

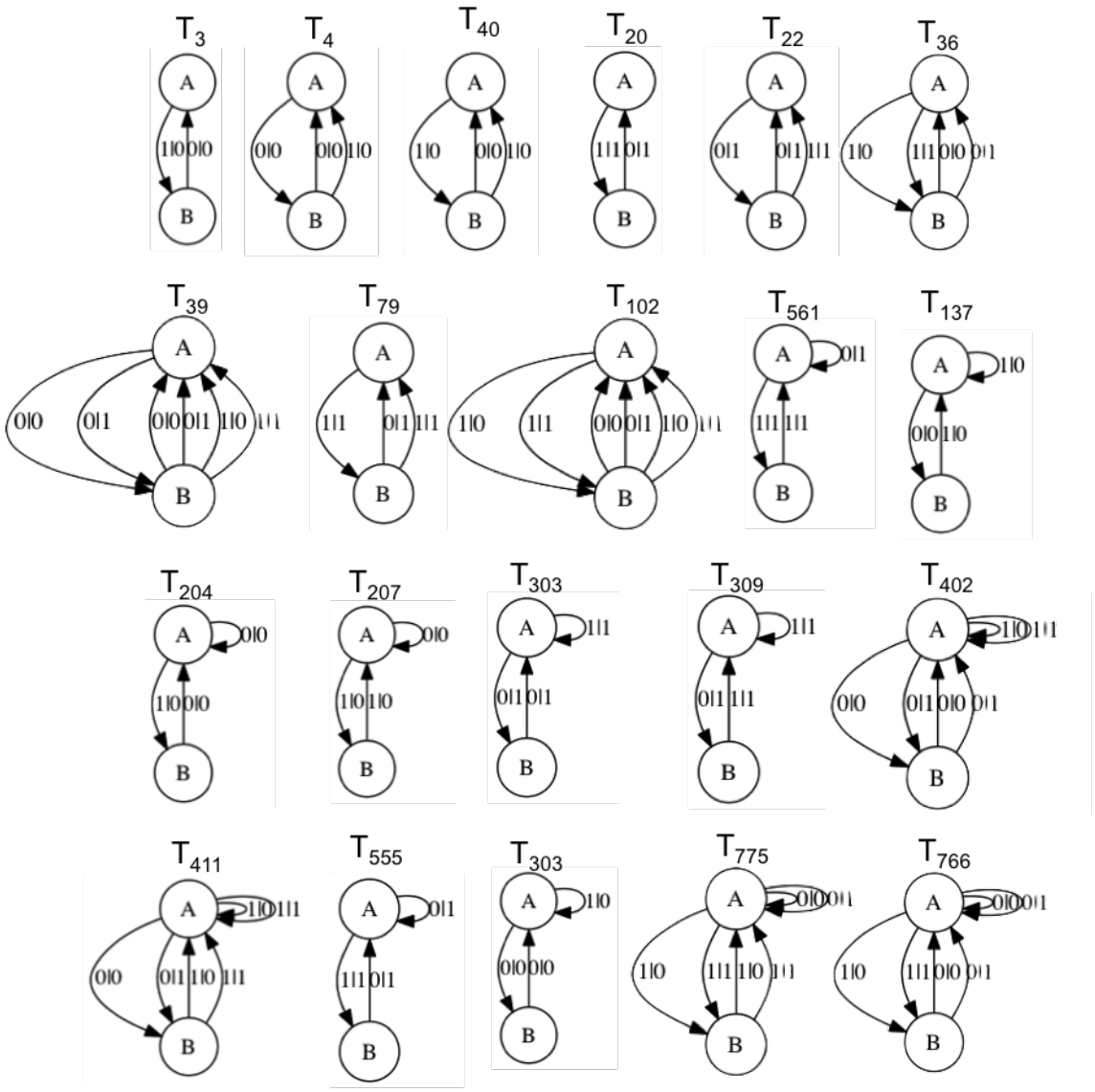


Figure 5.3: The 21 two-state automaton types that constituted niche 2*B*. The topology of this niche's automata were identical to those in niche 2*A* however each automata processed a different domain and range of binary information compared to their symmetrical twin in the other niche. Hence, whilst individual automata processed different information to their 'twin' in the other niche, as a collection of automata the niches 2*A* and 2*B* processed the same domain and range of binary information. Taken from [121].

interactions) producing the Slow Growth and Slow Decay automata. At the end of the simulation the 1,852 two-state automata that were initially present had gone extinct leading to a reduction in the interaction network complexity from 19.22 bits at $t = 0$ to 6.02 bits at $t = 2 \times 10^6$. Of those extinct automata 22.6% (424) were not produced at all and the remainder were produced in very low numbers and were eventually selected for removal from the population. An analysis of the interaction network indicated that it was heavily skewed towards producing a small number of automaton types in the population (see Table 5.2 and Figure 5.4).

As a large number of automata went extinct the interaction network complexity was drastically reduced. The number of interactions that were producing the niche automata were no longer possible as the automaton types that took part in those interactions were no longer present in the population. This led to the population becoming dominated by the automata that were part of strongly connected networks (i.e. mutually producing each other). Given that each automata in the competing niches were produced in equal number then the eventual dominance of one niche over the other was a function of the history of the productions that had occurred i.e. the incidental advantage conferred to one niche over the other was based on the chance that its constituent automata happened to have been produced more frequently up to that point.

Frequency of Production	No. of automaton types
0	424
1-300	1,313
301-600	76
601-900	10
901-1200	16
1201-1500	8
1501-1800	12
..	..
6001-6300	2
..	..
9601-9900	4
..	..
12001-12300	4
..	..
20001-23000	4

Table 5.2: The histogram of the number of productions that occurred in the interaction network and the number of automata that were produced in each bin. Analysis of the production of two-state automata showed that a very small number of automata (14 automaton types representing 0.2% of the population) were produced considerably more often than other automata.

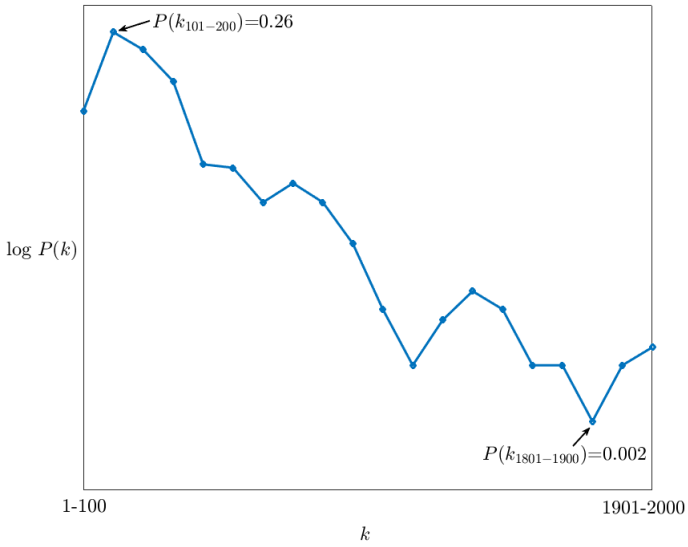


Figure 5.4: The degree distribution of the two-state interaction network. The x-axis was the k values (i.e. the total incoming and outgoing edges to/from each vertex in the network where a vertex represented an automata type) allocated into bins of width 100. The y-axis was the log $P(k)$ values for each of the k bins. The vast majority of vertices in the network had fewer than 200 edges whilst a very small number of vertices had a large number of edges (> 1,000) that indicated a heterogeneous network structure with a small number of highly connected 'hubs' [136].

The degree distribution varied significantly (see figure 5.4) and indicated a heterogeneous network structure that consisted of a large number of vertices with a hundred or so edges and a very small number of vertices that were highly connected (> 1,000 edges). In general, there was a direct relationship between an automaton's degree of connectedness and the frequency with which it was produced e.g. the small subset of automata that were highly connected and highly produced were members of the set of automata that constituted the niches $2A$ and $2B$. Figure 5.5 shows the topology of the interaction network for these niches after all other automata had gone extinct, and the population was in a steady-state.

5.3 Emergence of a two-state automata niche under zero-diffusivity conditions

A population of 90,000 two-state automata consisting of 1,873 unique types (with an average of 48 of each type) were randomly distributed on a 300 by 300 lattice and the simulation iterated for 5×10^7 iterations under environmental conditions of no diffusive

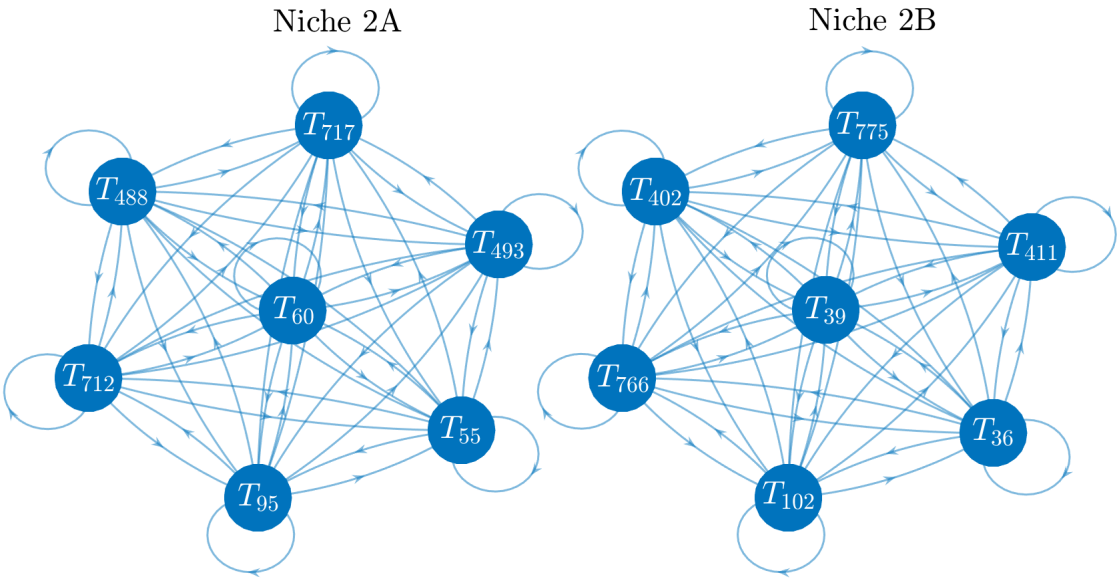


Figure 5.5: The competing interaction networks for niche $2A$ and $2B$. Each network had an identical topology that was a fully connected network consisting of seven vertices and 49 edges. Neither network held an intrinsic advantage over the other and the event that leads to the dominance of one set of automata occurred as a result of chance due to the stochastic nature of the random replacement mechanism of the information niche model.

mixing ($c = 0, v = 0$) and no influx of external automata ($\Phi = 0$). This resulted in the emergence of the niche $2C$.

The population followed the same trajectory as the well-mixed environment (niches $2A$ and $2B$) up to $t = 10^5$ after which there was a turning point with the previously low frequency automata from niches $2A$ and $2B$ growing rapidly to the detriment of the previously dominant automata (see Figure 5.6). The competition between niche $2A$ and niche $2B$ was not evident and appeared to have been neutralised by the lack of spatial mixing within the population. Subsequently, the 42 automata of niches $2A$ and $2B$ co-existed within a new steady-state structure representing the new niche $2C$. There were far fewer extinctions with 1,593 two-state automaton types remaining in the population (280 had gone extinct). This resulted in a higher interaction network complexity of $C_\mu(G) = 8.98$ bits compared to the $C_\mu(G) = 6.02$ bits of niche $2A$ or $2B$.

The niche $2C$ population transitioned through three phases. To aid in the analysis of the observed population dynamics the automata were allocated to five groups depending on their final frequency, in niche $2A$ or $2B$ and in niche $2C$ respectively, as shown in Table 5.3).

Phase 1 was characterised by the extremely fast growth of the automata groups A and B during the early stages of the simulation whilst the population was sufficiently well

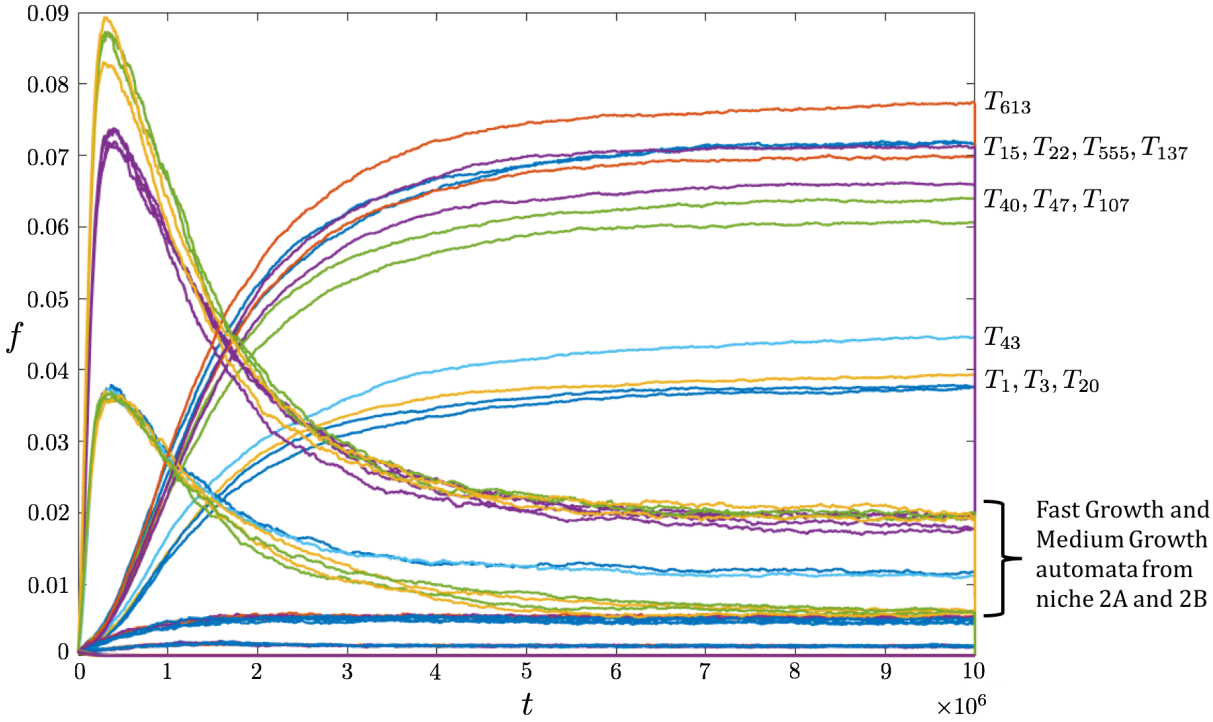


Figure 5.6: The population dynamics of a two-state automata population under conditions that emulated no diffusion ($c = 0, v = 0$) and which led to the emergence of a new niche ($2C$). In the first 2.5×10^5 iterations the population dynamics followed the same trajectory as niches $2A$ and $2B$ however there was a sharp turning point thereafter with the automata that constituted the 'Fast Growth' and 'Medium Growth' groups in the niche $2A$,$2B$ configurations experiencing rapid decay. The automata that constituted the 'No Growth' groups in niches $2A$,$2B$ here had instead experienced rapid growth into two groups - a dominant group consisting of the automata $T_{613}, T_{15}, T_{22}, T_{555}, T_{137}, T_{40}, T_{47}, T_{107}$ and a smaller group consisting of the automata T_{43}, T_1, T_3, T_{20}.

group	automaton types	frequency category in $2A$,$2B$	frequency category in $2C$
A	T_{39}, T_{60}, T_{95}, T_{102}, T_{411}, T_{493}, T_{712}, T_{775}	high frequency	low frequency
B	T_{36}, T_{55}, T_{402}, T_{488}, T_{717}, T_{766}	medium frequency	low frequency
C	T_{15}, T_{40}, T_{47}, T_{22}, T_{107}, T_{137}, T_{613}, T_{555}	low frequency	high frequency
D	T_1, T_3, T_{20}, T_{43}	low frequency	medium frequency
E	T_2, T_4, T_{81}, T_{79}, T_{106}, T_{561}, T_{120}, T_{204}, T_{121}, T_{207}, T_{417}, T_{303}, T_{421}, T_{309}, T_{617}, T_{134}	low frequency	low frequency

Table 5.3: The automata in the niches $2A$,$2B$ behaved differently under zero-diffusivity conditions. Analysis of the dynamics that was driving such different behaviour was aided by categorising the automata into the five groups ($A - E$) and determining the frequency category to which the automata in those groups belonged.

distributed across the lattice (thus re-producing the same dynamics as seen in the formation of niches $2A$ and $2B$). These automata groups quickly saturated the lattice where they were readily available for the automata in groups C and D to interact and from which the C,D automata reproduced themselves. In this way, the A,B groups were a food set for the C,D groups and this explained the growth in number of the automata in those latter groups (C and D). This was a one-way relationship - the automata in C,D only replicated themselves in all interactions with the automata in A,B. The lack of any spatial mixing, and the depletion of the A,B food set to produce more C,D automata, led to a marked reduction in the diversity of interactions that could take place. Over time the rate of change in the composition of the neighbourhood of each automata reduced significantly and this led to a reduction in the concentration of the A,B automata groups.

Phase 2 marked a rapid transition of the structure of the population with the sudden and rapid decay of automata in the groups A and B and the continued growth of the automata in the C and D groups. The production advantage of groups A and B - that they self-replicated in any interaction with other members of their group leading to a higher intensity of production - became a disadvantage as this required ready access to the other automata in their group which was severely curtailed by the zero diffusivity conditions set by the environment. By comparison, the automata in groups C and D continued to be produced by the automata in groups A and B even whilst those groups were decaying. This led to C,D replicated faster than other automata due to their self-replicative behaviour and this led to the formation of concentrated domains on the lattice that were constituted by a single type of automaton from the C or D groups. Simultaneously, these automata benefited from a 'replicate & lock-in' phenomenon whereby they did not readily interact with the other automata that shared the A,B food set. This non-interaction had the indirect effect of protecting the domains of C,D automata from being eroded through the gradual replacement at their periphery with different automaton types. This combination of maximising the food set of groups A,B in a one-way beneficial relationship to replicate themselves whilst not interacting readily with other C,D automata meant that these domains of automata were very robust structures on the lattice. Such a 'replicate and lock-in' mechanism proved to be an effective survival strategy. However, it was not the only survival mechanism observed - an interesting observation was that the A,B automata did not go extinct and this was due to a 'mutual maintenance' mechanism whereby these automata would mutually produce each other whilst also performing self-replication. This had the effect of maintaining a dynamic domain boundary between these domains that was able to partly counteract the 'replicate & lock-in' strategy of the automata in groups C

and D.

Phase 3 was characterised by the extinction of a large number of automata which significantly reduced the diversity of the interaction network. Consequently, the number of possible interactions with which to maintain the remaining population of automata were significantly reduced and parity was seen in the interaction network i.e. all of the remaining automata were produced in equal amounts. At this point the established domains of automata from groups A,B and C,D were able to maintain their concentration across the lattice through their respective competing processes of 'mutual maintenance' and 'replicate/lock-in' and this led to the emergence of the steady-state structure of niche $2C$.

Chapter 6 provides a more detailed explanation of the competing mechanisms and the spatial dynamics that led to the formation of niche $2C$.

5.4 Emergence of two-state automata niches under influx conditions

A population of 90,000 two-state automata consisting of 1,873 unique types (with an average of 48 of each type) were randomly distributed on a 300 by 300 lattice. Simulations were run for 5×10^7 iterations under environmental conditions of no diffusive mixing ($c = 0, v = 0$) and an influx of external automata at (i) a moderate rate ($0.1 < \Phi \leq 0.7$), (ii) a high rate ($0.7 < \Phi \leq 0.9$), and (iii) a very high rate ($0.9 < \Phi \leq 1$).

With the influx rate in the range $0 < \Phi \leq 0.7$ the niches $2A$ or $2B$ emerged albeit their formation was delayed when compared to an influx rate of $\Phi = 0$ (as described in section 5.2). The higher the influx rate the longer the delay in formation of the niche. A similar observation was made about the one-state population (see Chapter 4).

With the influx rate in the range $0.7 < \Phi \leq 0.9$ a new niche ($2D$) formed (see Figure 5.7). This niche was characterised by the co-existence / co-habitation of niches $2A$ and $2B$ on the lattice. The influx of automata had interrupted the intense competition in the earlier stages of evolution of the population and that would ordinarily lead to the eventual dominance of either $2A$ or $2B$ niche automata. Under these conditions all automaton types survived leading to a more complex population structure.

Finally, with $0.9 < \Phi \leq 1$ there was a lack of any structure in the population as the replacement of automata on the lattice was dominated by automata that had been randomly generated rather than selected from the existing population. This had the effect of negating

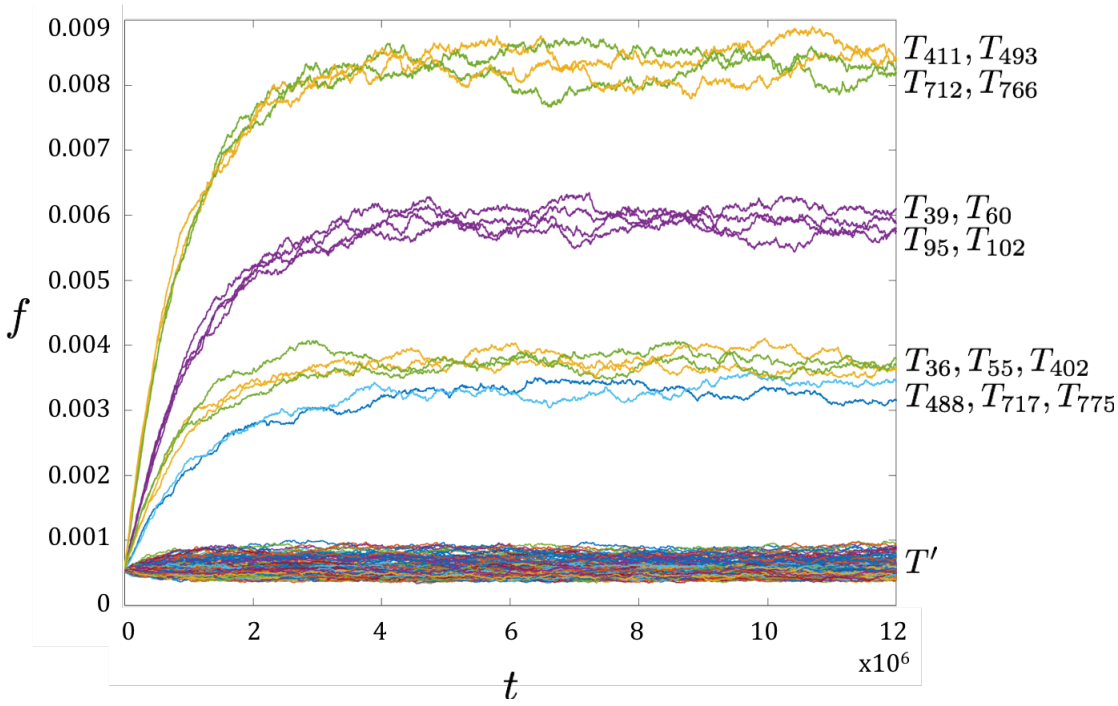


Figure 5.7: The emergence of niche $2D$ in the presence of an influx of external automata through random replacement at a rate $0.7 < \Phi \leq 0.9$ had the effect of neutralising the initial competition between the niche $2A$ and $2B$ automata leading to their co-existence in the population. The three clusters of automata that had undergone significant growth from $t = 0$ consisted of equal numbers of automata from niches $2A$ and $2B$ e.g. T_{411}, T_{712} from niche $2A$ and T_{493}, T_{766} from niche $2B$, and so on. T' represents all other automaton types in the population.

any structural 'memory' that the population could generate leading to an unstructured state. Whilst this state didn't represent a structured population, it was a possible state that could be reached by the population and, as such, was designated as niche $2E$ (see Figure 5.8).

5.5 Quantitative Analysis of Niche Structures

The information content and complexity of each niche was measured by calculating the average structural complexity ($C_\mu(T)$), the production threshold ($H(X)$) and the interaction network complexity ($C_\mu(G)$), respectively.

As can be seen from Table 5.4, niches $2A$ and $2B$ constitute a population of automata that were marginally of a higher average structural complexity compared to the other two-state niches. The range of structural complexity in the initial two-state population of 1,873 automaton types was $0.72 - 1$ bits. Table 5.5 shows the structural complexity

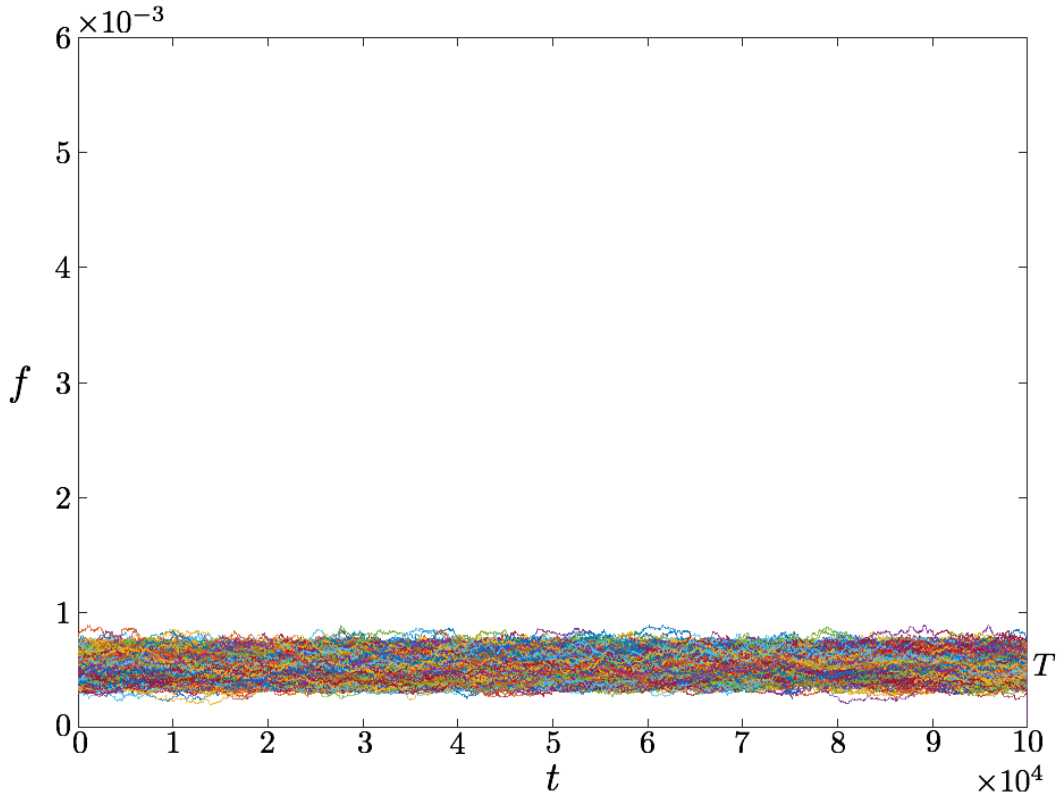


Figure 5.8: The emergence of niche $2E$ in the presence of a very high rate of influx of external automata through random replacement at a rate $0.9 < \Phi \leq 1$ and that led to an unstructured population. The majority of new automata that were being introduced into the population were generated randomly rather than being produced from the interactions of existing automata.

		niches				
	measure	$2A$	$2B$	$2C$	$2D$	$2E$
(a)	average structural complexity ($< C_\mu(T) >$)	0.95	0.95	0.94	0.94	0.94
(b)	production threshold ($H(X)$)	3.3	3.3	6.29	7.16	7.2
(c)	interaction network complexity ($C_\mu(G)$)	6.02	6.02	8.98	11.58	18.43

Table 5.4: Comparison of (a) the average structural complexity ($< C_\mu(T) >$) showing that the more highly structured niches consisted of marginally more complex automata, (b) the information content ($H(x)$) for each niche indicated an increase in the amount of information required to re-construct each niche as environmental disturbances were increased, and (c) the interaction network complexity $C_\mu(G)$ which was an overall measure of the complexity of a niche and, as can be seen, the complexity of the niches increase with changes in environmental conditions. All measures were generated using the final frequency distribution of the automata in each niche (i.e. the population structure) at a steady-state.

$C_\mu(T)$ bits	0.722	0.845	0.89	0.971	0.918	0.985	0.998	1
No. automata	56	168	48	48	408	432	368	345

Table 5.5: The structural complexity measurements of the two-state automata population were compartmented into eight discrete and well-defined classes. All automaton types in a class had an identical $C_\mu(T)$ value illustrating the structural diversity in the two-state automata population.

measurements of each automata type in the two-state population compartmented into eight discrete classes. By comparison, the range of structural complexity per automata in niches $2A$ or $2B$ were $0.92-1$ bits suggesting that these niche automata resided in the higher structural complexity classes. Given that 99% of the population went extinct as niches $2A$ and $2B$ formed it can be surmised that the lower structural complexity automata were removed from the population. Hence it was observed that the most highly structured niches consisted of a very small number of automata each of which had a higher-than-average structural complexity.

The production threshold - that is, the amount of information required to generate the niche - increased with the degree of environmental disturbance present during the formation of a niche. This was to be expected given that niches $2A$ and $2B$ consisted of only 21 automata each compared to the 1,593 automata present in niche $2C$, and the 1,873 automata present in niches $2D$ and $2E$.

Similarly, the interaction network complexity - the information required to describe the niche after it had evolved to a steady-state distribution and the possible interactions in that population - increased with the magnitude of environmental disturbance. The amount of structure in a niche was equated to the reduction in the interaction network complexity from the initial, unstructured two-state population ($C_\mu(G) = 18.43$ bits) to that of the steady-state niche population. For niches $2A$ or $2B$ this was 6.02 bits representing a reduction of 12.41 bits. The lower $C_\mu(G)$ value for niche $2D$ (11.58 bits) compared to $2E$ (18.43 bits) was due to the presence of more structure in niche $2D$.

5.6 Summary

This chapter has presented the results from simulating a two-state automata population evolving to five different information niches under various environmental conditions. The following niches were discovered:

1. Niche $2A$ or $2B$ emerged under well-mixed conditions, with the population undergoing an initial period of intense competition with two groups of 21 automata each emerging as highly competitive, strongly connected networks. These competing

groups co-existed up till $t = 2.5 \times 10^5$. At that point a sudden divergence occurred with one of the groups spontaneously undergoing rapid decay leaving the remaining group to grow and dominate the population. Repeated simulation runs revealed that either group of automata could come to dominate leading to the formation of either niche $2A$ or $2B$. The stochastic nature of the information niche model meant that it was not possible to predict which niche would be likely to emerge as the 'winner'. Both niches were robust and persisted even in the presence of a moderate influx ($0.1 \leq \Phi < 0.7$) of externally generated automata

2. Niche $2C$ emerged under low diffusivity conditions leading to the co-existence of the two groups of automata that had previously competed and that led to the formation of niche $2A$ or $2B$. However, the automata that had previously been poor competitors (i.e. underwent decay and eventual extinction) under well-mixed conditions now dominated the population leading to the emergence of a new steady-state structure that represented a new niche ($2C$). Two competing mechanisms were identified - the 'replicate & lock-in' and 'mutual maintenance' processes - which were not observed in the one-state information niche simulations. This suggested that a population with a higher average structural complexity generated concurrent mechanisms of competition and survival that led to more complex competitive dynamics. These mechanisms are explored in more detail in Chapter 6.

3. A high level of influx of externally generated automata ($0.7 \leq \Phi \leq 0.9$) had the effect of neutralising the competition between the two competing niches ($2A$,$2B$) leading to their co-existence in the population. The resulting steady-state organisation was designated as niche $2D$.

4. With a very high rate of influx of external automata ($0.9 < \Phi \leq 1$) the degree of disturbance was such that no structure emerged in the population. This was due to the loss of any 'history' of the populations endogenous productions meaning that no single automata could maintain its growth trajectory. The converse was also true in that this also meant that uncompetitive automata could also not maintain a decay trajectory. The result was a homogenous state of the population known as niche $2E$.

Furthermore, the following general observations were made:

1. Two highly competitive automata groups emerged whose interaction networks had the following properties: (i) strongly connected topology where each member of the network was produced by other members of the network; and (ii) dynamically stable

with no constituent members going extinct. This was consistent with the findings from simulating the information niche model with a simpler, one-state population of automata (see Chapter 4).

2. A two-state population of automata had a higher average structural complexity that produced more complex population dynamics than a one-state population that had zero structural complexity. For example, the two highly competitive groups of automata that emerged to form niche $2A$ or $2B$ could co-exist under conditions where there was a high rate of influx ($0.7 \leq \Phi \leq 0.9$) of externally generated automata, whilst they competed intensely until the 'death' of one of groups under well-mixed ($c = N, v = n$) and closed conditions ($\Phi = 0$). This may indicate that increasingly complex automata populations are able to support multiple niches simultaneously. This is discussed further in Chapter 10.

3. The information niche model with a significantly larger and more diverse population did not generate an increased number of distinct niches for the range of environmental conditions simulated e.g. the one-state and two-state automata simulations both identified five distinct niches under fixed environmental conditions. The two environmental parameters used to simulate environmental disturbances - spatial mixing (c, v) and an influx (Φ) of externally generated automata - may have constrained an exhaustive examination of the theoretical range of possible structural states of a two-state population under the influence of an environment. This is discussed further in Chapter 10.

CHAPTER 6

RESULTS III - SPATIAL PATTERNS

6.1 Introduction

This chapter presents the results of investigating the spatial patterns that formed on the lattice (Γ) during the formation of one-state and two-state information niches under certain environmental conditions. Niche $1B$ from the one-state population and niche $2C$ from the two-state population emerged under non-diffusive conditions and were of particular interest as their lattice configurations demonstrated domain and boundary patterns and dynamics. This was of interest as autopoietic theory requires the formation of compartmented structures [9] and, whilst this requirement is debatable (as discussed in Chapter 10), the formation of such structures in niches $1B$ and $2C$ warranted further investigation.

6.2 Pattern formation on the lattice of a one-state information niche

The spatial configuration and topological structure associated with the emergence of the steady state niche $1B$ produced in the absence of lattice site ($\Gamma_{i,j}$) diffusion ($c = 0, v = 0$) and no influx of randomly generated automata ($\Phi = 0$) was investigated. A distinct spatial configuration was associated with niche $1B$ (see Figure 6.1a) compared with information niches $1A$, $1C$ and $1D$, which showed no spatial structure due to lattice diffusivity (see

Figure 6.1b). This result was similar to that reported in [123].

Amongst the automata in niche $1C$, the high frequency (T_2, T_4) group was de-mixed into a bi-continuous structure of T_2- and T_4-rich domains that were separated by a thin boundary layer comprising the low frequency population of T_1 and T_8 automata. The latter formed specifically at the interface due to the non-commutative functional compositions: $T_2 \circ T_4 = T_1$ and $T_4 \circ T_2 = T_8$. Growth of the T_2- and T_4-rich domains occurred through the generation of new automata specifically in the boundary regions comprising an interfacial 'double-layer', and was associated with continuous repair of the (T_1,T_8) boundary (as illustrated in Figure 6.1c-f).

Figure 6.1 illustrates the expansion of domains via. the outward growth of a boundary. In niche $1B$ only four automaton types remained from a population of 15 automaton types. Under well-mixed conditions these automata experienced no growth and only maintained their initial concentration in the population. However, under zero diffusivity conditions these automata became very competitive and came to dominate the population with the extinction of the other 11 automaton types. Repeated simulations indicated that the eventual configuration of the lattice was primarily due to the stochastic nature of the replication process and the initial random configuration of the automata on the lattice at $t = 0$.

Figure 6.2 illustrates the domain and boundary characteristics of the four automata T_1,T_2,T_4,T_8 that emerged uniquely under low diffusivity environmental conditions. In this configuration setting the T_2, T_4 (domain) automata constituted distinct contiguous domains on the lattice and the T_1, T_8 (boundary) automata formed at the interface between domains to form a boundary that bisected those domains. Specifically:

- T_1,T_8 self-replicated and were self-sustaining along the interface between the T_2 and T_4 domains
- T_1 was created by the interaction of the domain automata T_2 with T_4 (as per the non-commutative relationship: $T_2 \circ T_4 = T_1$) and hence wherever those two domains came into direct contact the boundary automaton T_1 was produced
- T_2 was created from the interaction of T_8 with itself and also between T_1 and itself. As such, formation of the T_2 domain was dependent on the presence of boundary automata
- T_4 was created from the interaction of T_8 and itself and also between T_1 and itself. As such, the formation of T_4 was dependent on the presence of boundary automata

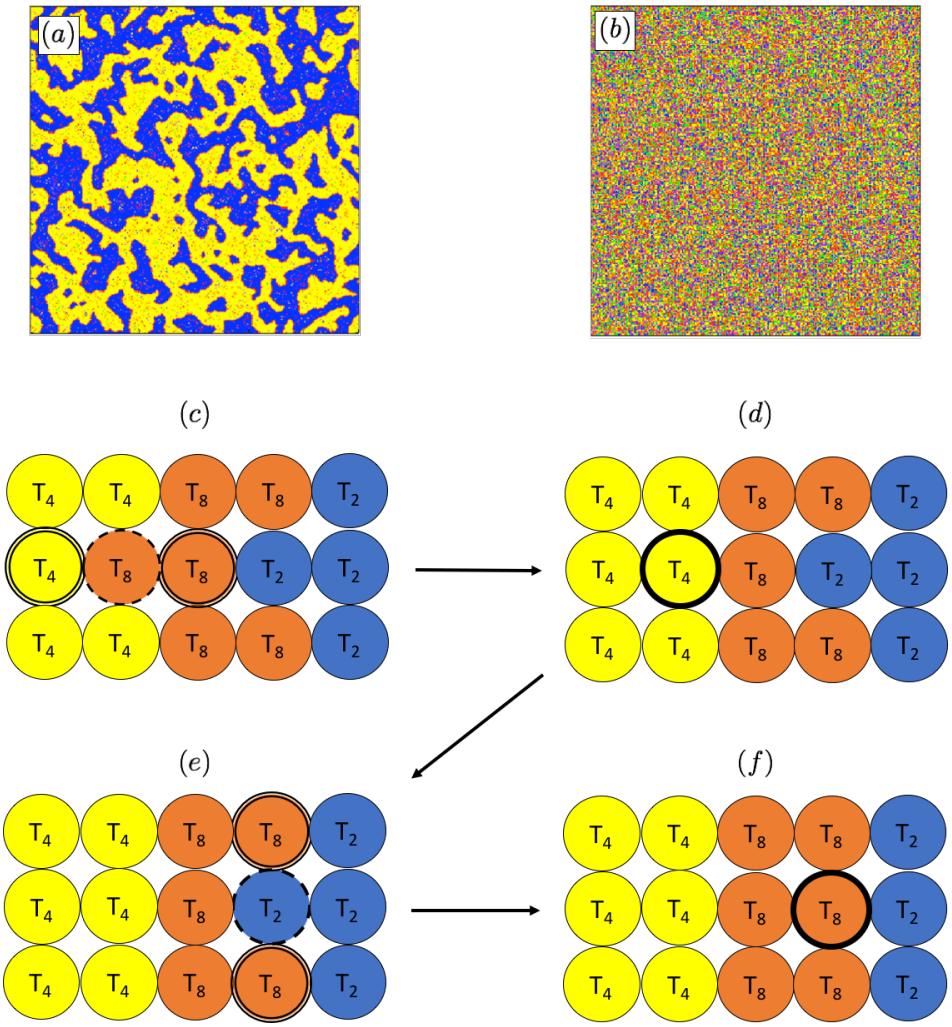
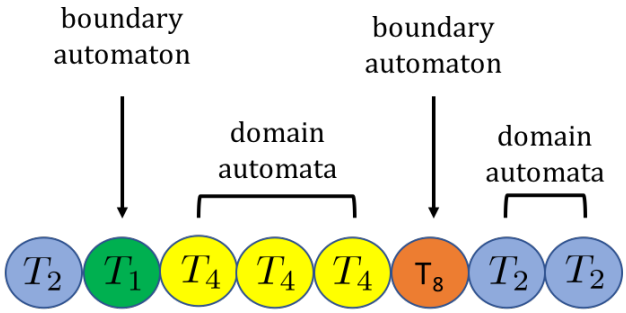


Figure 6.1: (a) Colour coded map showing the spatial configuration of the lattice of niche $1B$. A distinct topological structure consisting of a bi-continuous arrangement of T_2(blue)- and T_4(yellow)-rich domains separated by a thin interfacial layer of T_1 (red) and T_8 (orange) automata are shown; lattice x and y axes ran from $1 \rightarrow n$ from the top-left corner to the bottom-right, and (x,y) provided a unique index for each automaton sited on the lattice $\Gamma_{x,y}$; (b) the colour-coded map for niches $1A$, $1C$, or $1D$ showing no spatial structure on the lattice due to the presence of spatial mixing. (c-f) Example of lattice domain growth (c,d) and boundary repair (e,f) for niche $1B$: (c) a boundary automaton of different type to the adjacent domain automaton (T_8; dashed circle) was randomly selected for replacement, and the interacting neighbours selected with a 25% probability to perform the functional composition $T_8 \circ T_4$ (double circles); (d) As $T_8 \circ T_4 = T_4$, automaton T_4 replaced T_8, leading to an increase in the size and coherence of the T_4 domain; (e) in a later iteration, a T_2 domain automaton, surrounded by three boundary automata, was randomly selected to be replaced (dashed circle) and the selected interacting neighbours were $T_8 \circ T_8$ (double circles); (f) As $T_8 \circ T_8 = T_8$, automaton T_2 was replaced by T_8, repairing the boundary and shrinking of the adjacent domain. Whilst growth of a domain produced a temporary decay in the boundary, the defects were subsequently repaired at the expense of other automata in adjacent domains. This dynamic produced a bi-continuous spatial configuration after 10^7 iterations as shown in (a). However, over a very large number of iterations ($t >> 10^7$), either the T_2 or T_4 domain completely dominated the lattice, resulting in extinction of all other automaton types and the formation of a homogeneous population.



$$T_2 \circ T_4 = T_1$$
$$T_2 \circ T_8 = T_2$$
$$T_8 \circ T_4 = T_4$$
$$T_4 \circ T_2 = T_8$$

Figure 6.2: A one-dimensional extract of the lattice illustrating the spatial configuration of niche 1B that consisted of four automaton types that - due to their relationships - led to the emergence of two complementary behaviours of domain automata (T_2,T_4) and boundary automata (T_1,T_8).

- T_8 was created by the interaction of T_4 and T_2 ($T_4 \circ T_2 = T_8$) and hence wherever those two domains came into direct contact the boundary automaton T_8 was produced

Hence, T_2 and T_4 did not produce each other however they did participate in maintaining the boundary automata between their respective domains. These four automaton types formed an elementary network (i.e. dynamically stable, strongly connected and irreducible - see Chapter 4) that was unique in a one-state population; its constituent automaton types were the only combination of automata that produced each other in a manner whereby each domain automaton could produce a boundary automaton but it could not produce itself nor the other domain automaton. Furthermore a boundary automaton could produce themselves and a domain automaton. This led to the 'protected outgrowth' of each domain because (a) decay of a domain could only occur via. boundary dynamics and hence the interior of each domain was protected from being directly changed, and (b) the encroachment of a boundary into another domain enabled the other (competing) domain to expand into the space created by the extension of the boundary (as illustrated in Figure 6.1c-f). Hence, from the unique relationships between these four automata - that were also competing with each other[1] - a survival strategy emerged. This survival strategy, of domain growth facilitated through a continually maintained and expanding boundary, required co-operation between this subset of automata and that was subsequently termed 'protected outgrowth'. There was no evidence of the emergence of alternative competitive strategies from the interaction networks of other one-state automaton types operating under zero-diffusivity conditions and such automata were subsequently expelled from the population.

[1]This may seem to contradict the co-operative behaviour seen in niche 1B however competition between automata for survival was present and this was demonstrated where either the T_2 or T_4 automata would come to dominate and homogenise the lattice. Such occurrences required extended timescales (i.e. 10^8 iterations).

6.3 Pattern formation on the lattice of a two-state information niche

The spatial configuration and topological structure associated with the emergence of the steady state niche $2C$ which emerged in an environment that was absent of lattice site diffusion ($c = 0, v = 0$) and no influx of randomly generated automata ($\Phi = 0$) was investigated. Domains enriched with single automaton types were evident on the lattice. Further examination of the lattice did not indicate the presence of any boundary-type automata similar to those that had been observed in niche $1B$. Instead the domains were in direct contact with each other (see Figures 6.3 and 6.4).

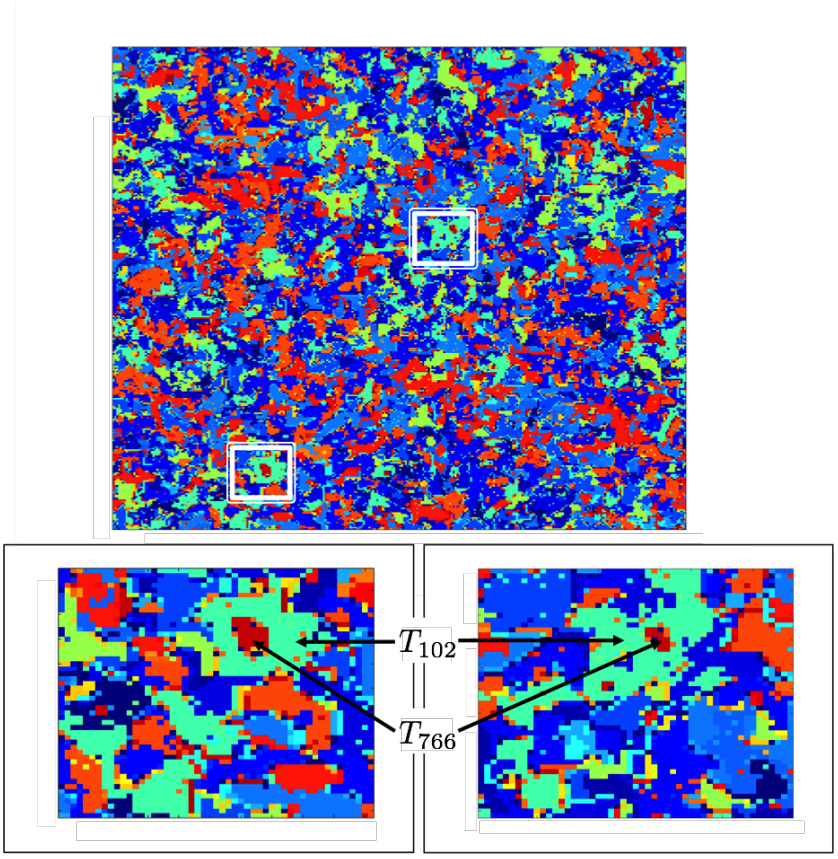


Figure 6.3: The spatial patterns of the lattice for the niche $2C$ at 5×10^6 showing two areas of interest where T_{766} automaton types were surrounded by T_{102} automata. Examination of the changes in the lattice at this location over successive time-steps, along with an analysis of the interaction network between these automata, indicated the presence of the 'mutual maintenance' survival mechanism. Taken from [121].

Large regions of homogenous domains of automaton types formed from two competing survival mechanisms (see Table 6.1 for the list of two-state automaton types that

constituted these domains):

(a) automata that had the ability to self-replicate and to mutually produce other self-replicators. Examination of the lattice revealed the motif of a domain surrounded by another domain (see Figure 6.3). This compartmentation of the interior domain was a result of two domains of automata mutually producing each other at their interface whilst simultaneously self-replicating within their interior (see Figure 6.7). This proved to be a reasonable survival strategy and the automata exhibiting such 'mutual maintenance' behaviour remained in the population albeit at a low frequency.

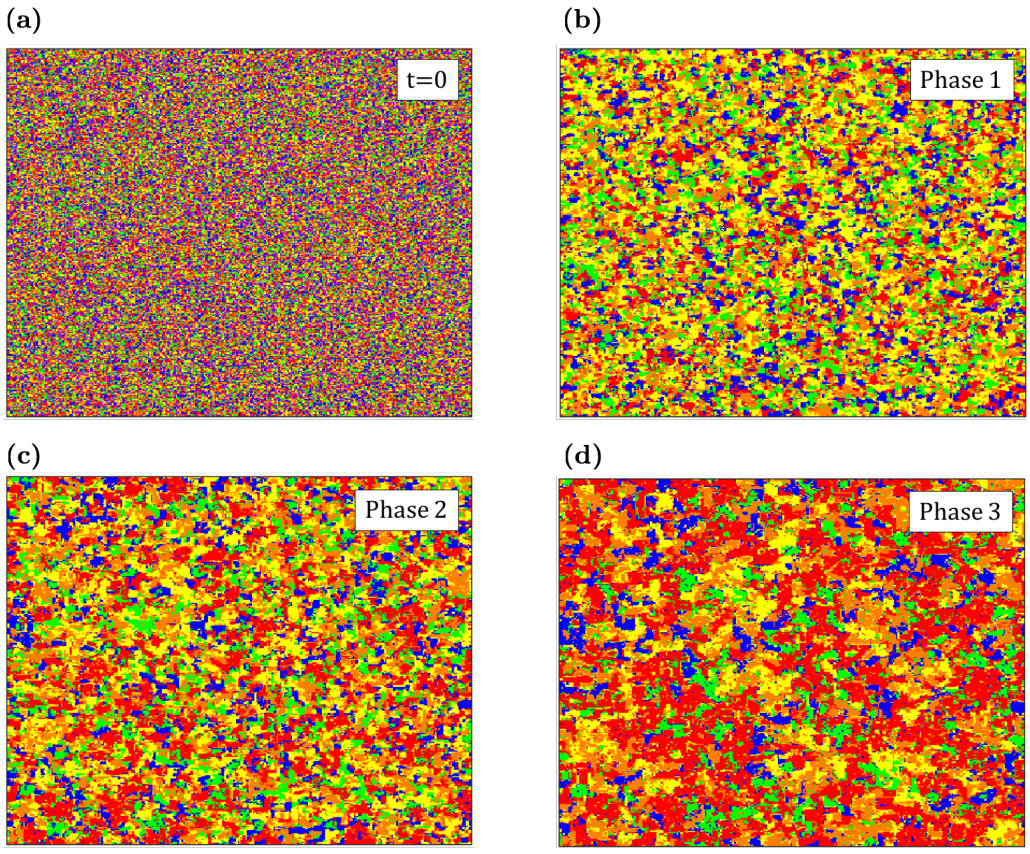


Figure 6.4: Evolution of niche 2C illustrated by the spatial patterns during the three different phases of the population: (a) the state of the lattice at $t = 0$ with the 1,873 two-state automaton types randomly distributed across the 300 by 300 lattice; (b) the lattice at $t = 0.5 \times 10^6$ (Phase 1) indicating the peak of concentration of the small subset of 14 automaton types that self-replicated and mutually produced each other ('mutual maintenance' automata shown as yellow regions), (c) the lattice at the start of the crossover point (Phase 2 at $t = 1.5 \times 10^6$) where the dominant automata from Phase 1 had decayed significantly as they were used as the food set for the production of the 'replicate & lock-in' automata which had now replaced them as the dominant automata in the niche (red, orange and blue regions), and (d) the final state of the lattice at $t = 10^7$ (Phase 3) with dominance of the lattice by the 'replicate & lock-in' automata.

(b) automata that used the automata in (a) as a food set to produce themselves in non-reciprocal interactions thus leading to their outgrowth from a 'seeded' location on the lattice. This growth continued whilst there was either a sufficient food set available in the neighbouring lattice sites, or until the outer edges of the domain met another domain with which it could not interact thus forming a hard domain boundary (see Figure 6.6). Such domain boundaries were characterised as a mutually exclusive region between two domains i.e. no possible interactions existed between the adjacent domain automata and therefore no new automata could be produced at the interface between those domains. Once a domain was surrounded by other automata with which it could not interact no further growth - nor decay - of the domain was possible. In this way, and over time, all of the domains of this type became locked in. This 'replicate & lock-in' mechanism of domain growth followed by exclusion emerged as a survival strategy and participating automata came to dominate the niche.

These concurrent mechanisms of survival in the niche - 'replicate & lock-in' and 'mutual maintenance' - were in competition throughout the formation of niche $2C$. As the population precipitated on the lattice (i.e. the frequency of changes to and the diversity of the neighbourhood of each automaton decreased as the simulation progressed) the selfish behaviour of the 'replicate & lock-in' automata became more effective (see Figure 6.5).

By comparison, the 'mutual maintenance' automata were dependent on the presence of other automata in their neighbourhood that supported such a survival mechanism (see Figure 6.7). The time-series data for a simulation of niche $2C$ (see Figure 6.5) revealed how this competition typically unfolded with the initial, rapid growth of the 'mutual maintenance' automata during Phase 1 providing a rich food set for the 'replicate & lock-in' automata that subsequently experience rapid growth in Phase 2 leading to the displacement of the 'mutual maintenance' automata. This culminated in the precipitation of the lattice during Phase 3 characterised by a population dominated by domains of 'replicate & lock-in' automata.

Survival Mode	Participating automaton types
Mutual maintenance	$T_{36}, T_{39}, T_{55}, T_{60}, T_{95}, T_{102}, T_{402}$, $T_{411}, T_{488}, T_{493}, T_{712}, T_{717}, T_{766}, T_{775}$
Replicate & Lock-In	$T_1, T_3, T_{15}, T_{20}, T_{22}, T_{40}, T_{45}, T_{47}, T_{107}, T_{134}, T_{137}, T_{555}, T_{613}, T_{617}$

Table 6.1: The automaton types that participated in the 'Replicate & Lock-In' and 'Mutual Maintenance' survival mechanisms in a two-state automata population operating under zero diffusivity ($c = 0$, $v = 0$, $\Phi = 0$) environmental conditions.

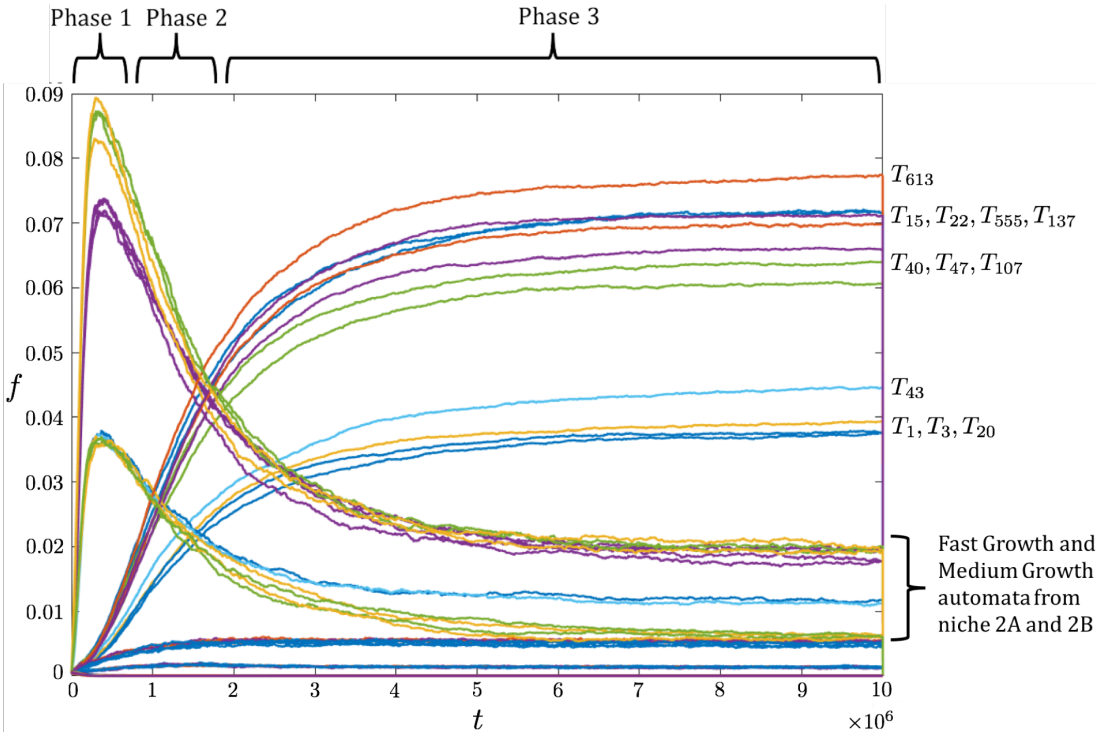


Figure 6.5: The time-series of the frequency distribution of the population indicating the three phases (1 - 3) through which the population evolved to form niche 2C.

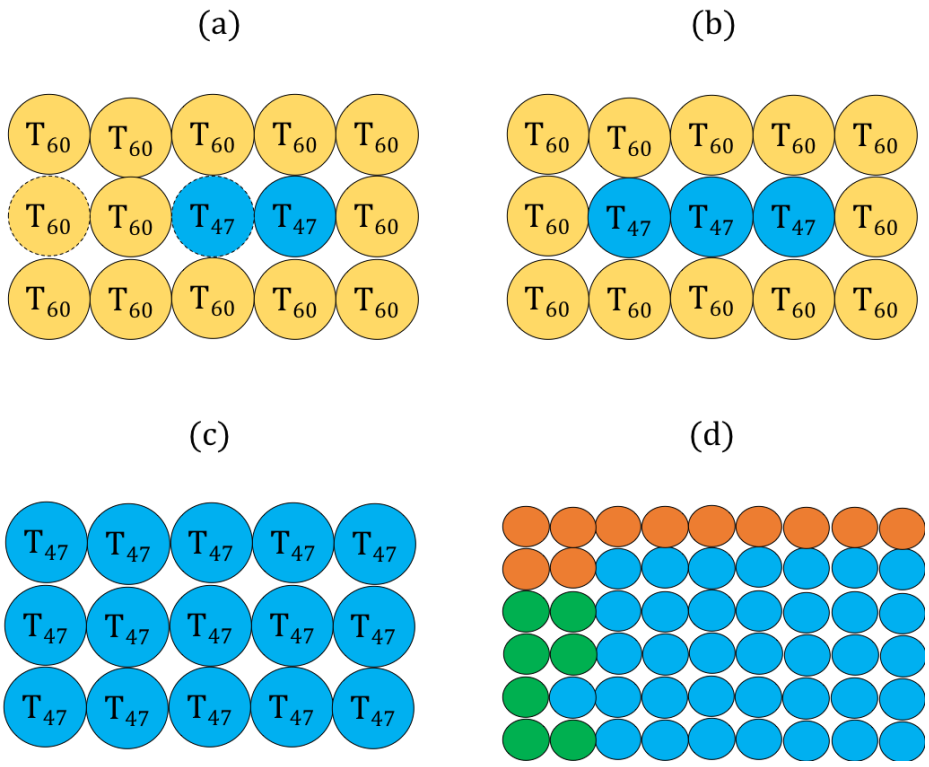


Figure 6.6: Illustration of the *replicate & lock-in* strategy that emerged during the simulation: (a) the T_{60} automata are self-replicators and were rapidly produced in the earlier stages of the simulation and became highly concentrated on the lattice. Here the T_{60} automata have surrounded the T_{47} automata which are a network replicator (i.e. T_{47} needed to interact with other automata apart from itself to produce itself); (b) in any interaction between these two automata the T_{47} automata were produced and replaced the T_{60} automata as illustrated here; (c) this outward growth of the T_{47} automata into a T_{60} rich lattice continued with the T_{60} automata acting as a food set; and (d) this process continued until the T_{47} domain (illustrated as blue circles) met other domains (illustrated as orange and green circles) consisting of automata that were also using the T_{60} type automata as a food set. Where these domains met the growth of their domains ceased as their constituent automata could not interact with each other thus rendering these domains effectively 'locked in' and with no further growth of the domain possible at the boundary with the opposing domain.

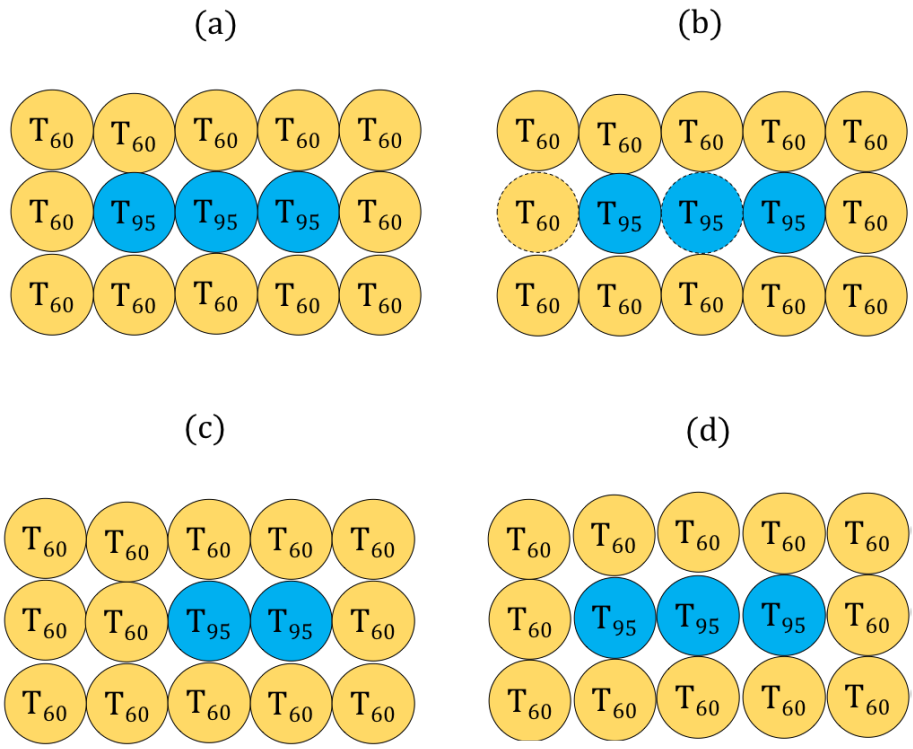


Figure 6.7: Illustration of the *mutual maintenance* strategy that emerged for a small group of automata under conditions of low diffusivity on the lattice. The example automata here are T_{60} and T_{95}, which self-replicated and produced each other in all interactions between them: (a) a small subsection of the lattice illustrating the T_{60} automaton type surrounding the T_{95} automata, (b) two automata are selected (as indicated by the dashed lines) to interact according to $T_{60} \circ T_{95} = T_{60}$, (c) the interaction produced a new T_{60} automaton which replaced the T_{95} automaton that was previously at that location, and (d) a sample of the same sub-section of the lattice at a later point in time indicated that the T_{95} automaton had now successfully replicated itself in its interactions with the T_{60} automata according to $T_{95} \circ T_{60} = T_{95}$.

6.4 Summary

This chapter has examined the spatial patterns that form on the two-dimensional lattice of the one-state information niche 1B and the two-state information niche 2C both of which emerged under low-diffusivity environmental conditions ($c = 0$, $v = 0$, $\Phi = 0$). Both niches formed elaborate spatial patterns on the lattice that were characteristic of distinct domains and boundaries between those domains.

- Niche 1B formed two domains composed of automata T_2 or T_4 that competed through a mechanism of 'protected outgrowth' whereby each domain is seeking to extend its boundary via. production of the boundary automata (T_1,T_8) into the lattice sites of an adjacent, competing domain. This competitive process led to the formation

of complex spatial patterns that were reminiscent of those discovered in physical systems such as spinodal decomposition (see Chapter 10). The non-trivial dynamics that led to the evolution of such spatial patterns were surprising given that a very small population of just four automata was responsible for such complexity.

- Niche $2C$ formed domains of automata that were not composed of any boundary automata. Rather the domains were immediately adjacent to each other. Two competing mechanisms were identified - 'replicate & lock-in' and 'mutual maintenance' - with the automata that were part of the former the most competitive and that came to dominate the population. The automata operating as part of the 'mutual maintenance' mechanism were still present in the population over extended periods of time and, hence, were judged to be operating an effective survival strategy. Both of these mechanisms arose as a result of the intrinsic information processing capability of different automaton types and the relationships between them.

- Automata operating the 'replicate & lock-in' strategy would produce themselves in the vast majority of interactions with other automata and, critical to their success, in any interaction with the group of automata that grew exponentially in the early stages (Phase 1) of the simulation. This rich food set of self-replicating and fast growing automata rapidly populated the lattice, however, as they met the 'replicate & lock-in' automata they were unable to compete as they were transformed into 'replicate & lock-in' automata without any reciprocation. This led to the rapid growth of 'replicate & lock-in' domains that proceeded until these domains reached other 'replicate & lock-in' domains with which they were unable to interact. This resulted in mutually exclusive zones of production at the interface of these domains that prevented further growth of those domains (hence the 'lock-in' aspect of this mechanism).

- By comparison, the 'mutual maintenance' domains consisted of self-replicators that were effective at dynamically reproducing other self-replicating automata domains at their point of contact. This had the effect of maintaining domains of self-replicators in proximity to other self-replicating domains. However, this was not an effective strategy for expanding the domains across the lattice but it was an effective strategy for protecting and maintaining such co-operating domains in the population albeit in very small numbers.

- The information niche model has demonstrated non-trivial spatial patterning on the lattice in a one-state and two-state automata population. Three novel, competing mechanisms emerged through the intrinsic information processing nature of the

automata and the relationships between them and these directly led to the formation of the spatial patterns observed. Whether a two-dimensional lattice with discrete, fixed locations for automata was a constraint on all possible spatial dynamics of a one-state or two-state automata population is discussed in Chapter 10.

CHAPTER 7

RESULTS IV - INTERACTING ONE-STATE AND TWO-STATE INFORMATION NICHES

7.1 Introduction

A key characteristic of an autopoietic system is its ability to maintain its identity in the presence of external disturbances. The process by which it is proposed to do this is called cognition [7] which can be decomposed into two steps [12] (see Figure 7.1):

1. Assimilation. A change in the internal structure of the system via. the absorption in some way of elements that are presently external to the entity and their subsequent integration into the inner processes of the entity, whilst maintaining the original identity and viability of the system. This process is termed assimilation and it leads to a *temporary* change in the entity's structure without any loss of its global organisation. Entities that are able to contribute to the production processes are said to be actively assimilated whilst those entities that are more neutral and non-participatory are deemed to be passively assimilated with the latter type eventually being expelled from the system [13].

2. Accommodation (or Adaptation as per [12]). A disturbance that permanently changes the autopoietic system and leads to a re-organisation of the system. This *discrete evolution* of the autopoietic system [7] equips the recently modified system to process further disturbances of the same kind in a more efficient way. The re-organisation must continue to re-generate an autopoietic system.

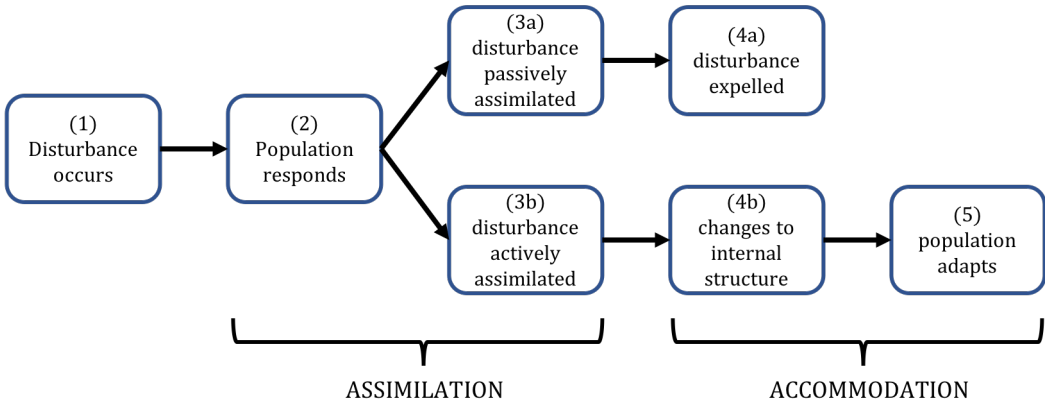


Figure 7.1: The cognition process [12] within the context of an automata population indicating the two types of adaptation that can occur: (a) assimilation where a new entity or disturbance becomes part of the structure of the system without changing its overall organisation, and (b) accommodation where a new entity or disturbance triggers a re-organisation of the system without its loss of identity as an autopoietic system.

This chapter is part one of a two part investigation into cognition in a self-producing population of one-state and two-state automata. The focus of these simulations was on the effect of material disturbances either through the influx of externally generated automata from an established neighbouring niche or the co-location of automata from two previously separate populations. Two specific questions were posed: (i) does the identity of either a one-state or two-state niche re-generate and emerge even when co-located with other automata?; and (ii) does the identity of an established niche maintain itself or is it lost in the presence of material disturbances?

The second part of investigating cognition is covered in Chapter 8 which examined the effect of endogenous and exogenous information flows on the formation of a one-state niche.

7.2 Simulation Set-up

Two developments were required to the information niche model:

1. Allow an influx of automata from an established two-state niche ($2A$) into an existing one-state niche ($1A$). A two-state population under well-mixed conditions was generated to a steady-state structure that corresponded to niche $2A$ (see chapter 5). In addition, a one-state population under well-mixed conditions was also generated to a steady-state structure that corresponded to niche $1A$ (see chapter 4). The simulation model was extended to handle the productions that arose from the interactions between the one-state and the inflow of two-state automata that constituted these

separate niches. The model was configured so that there was a unidirectional flow of two-state automata into the one-state population.

2. Allow the co-location of one-state/two-state (joint) automata populations on the same lattice. This required the *a priori* generation of a joint interaction network matrix (G_{joint}) to capture all possible interactions between the 1,888 automaton types (15 one-state and 1,873 two-state automata) in the joint population.

Once these enhancements were developed and tested the following simulations were performed:

- Simulation of an intermixed, joint one-state and two-state population consisting of 1,888 automaton types under well-mixed (see section 7.3) and low diffusivity conditions (see section 7.4)
- Automata from the niche $1A$ consisting of nine one-state automata combined with the automata of the niche $2A$ consisting of 21 two-state automata simulated firstly from an initially uniform distribution of automata (see section 7.5) and secondly where the initial distribution of automata corresponded to their original compositions in their original niche configurations (see section 7.6)
- An established two-state automata niche $2A$ disturbing the one-state niche $1A$ via. the influx of single two-state automata per time step at a rate $\Phi = 0.5$ (see section 7.7)

7.3 The dynamics of a joint one-state/two-state population under well-mixed conditions

The joint population consisted of all 15 one-state automaton types ($T_1..T_{15}$) and all 1,873 two-state automaton types ($T_{16}..T_{1888}$)[1] representing a total of 1,888 unique automaton types. An interaction matrix G_{joint} was generated that identified 400,744 interactions between all one-state and two-state automata: 207 of those interactions were exclusively between one-state automata, 355,484 interactions were exclusively between two-state automata and 45,053 interactions were new interactions between one-state and two-state automata. In all cases only interactions that produced one-state and two-state

[1]The indexing used to identify each unique automata type was $i = 1 \rightarrow 1,8888$ and so automata type T_{16} in the joint population corresponded to the two-state automata type T_1 and automata type T_{1888} corresponded to the two-state automata type T_{1873} from the two-state population as per Chapter 5.

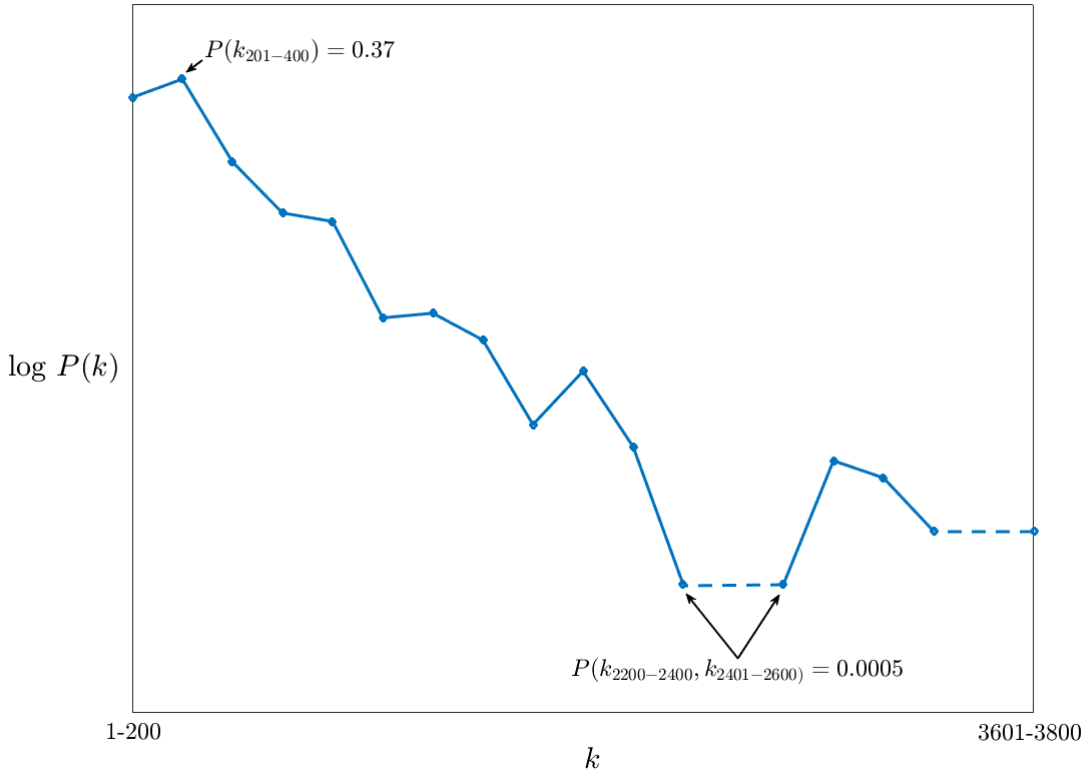


Figure 7.2: The degree distribution of the joint one-state/two-state interaction network. The x-axis were the k values (the incoming and outgoing edges from each vertex in the network) allocated into bins of width 200. The y-axis were the log $P(k)$ values for each of the k bins. As can be seen the large majority of vertices in the network had fewer than 400 edges whilst a very small number of vertices had a large number of edges indicating a heterogeneous network structure with a small number of highly connected 'hubs' [136]. Compared to an exclusively two-state interaction network the joint one-state/two-state network had more hubs with > 2,000 edges due to the inclusion of the one-state automata which constituted these highly connected vertices in the network.

automata were allowed and added to the joint interaction matrix. The characteristics of this interaction network is shown in Figure 7.2.

The joint one-state/two-state population had an initial interaction network complexity of $C_\mu(G_{joint}) = 18.61$ bits, an average structural complexity of $< C_\mu(T) >= 0.93$ bits and a production threshold of $H(X) = 3.9$ bits. The population was distributed across a 300 by 300 lattice with an average count of 48 of each type of automata. The simulation was run under well-mixed conditions ($c = N, v = n, \Phi = 0$ where N was the population size and n the width of the lattice) for 10^7 iterations (see Figure 7.3).

From an initial population of 1,888 automaton types only 35 automaton types remained

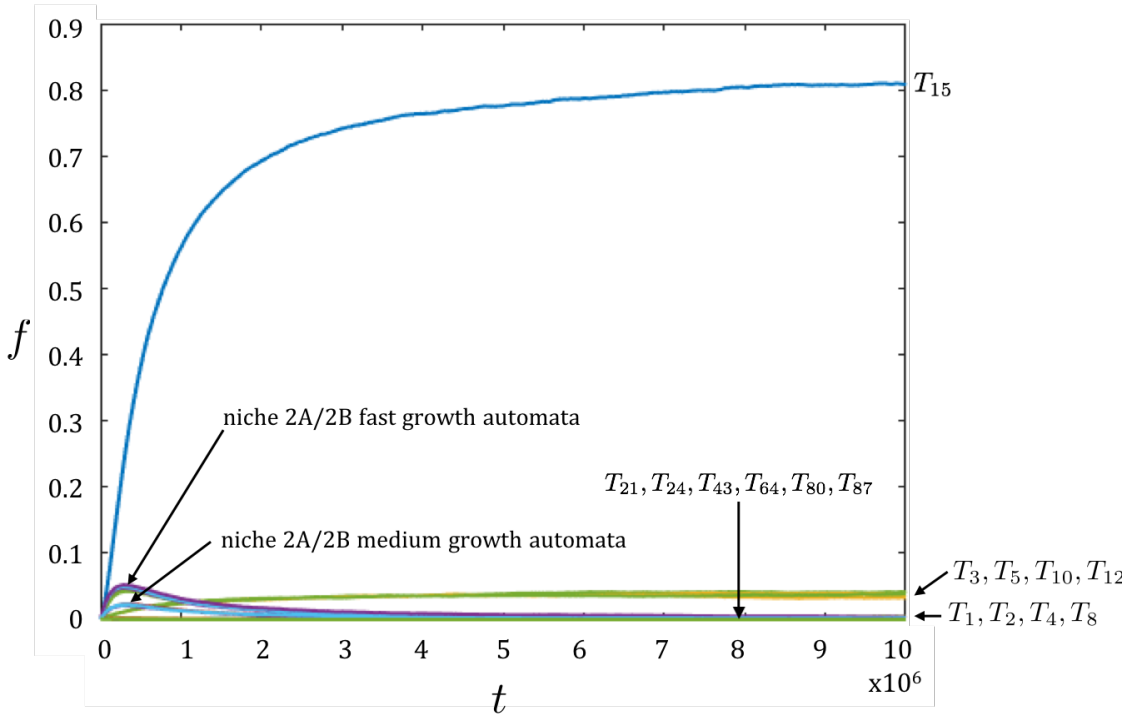


Figure 7.3: A graph showing the time-series frequency distribution of the joint one-state/two-state population over 10^7 iterations showing that: (i) the one-state niche ($1A$) was reproduced albeit with a different structure that accentuated the frequency gap between the four automata clusters 'Fast Growth' (T_{15}),'Slow Growth' (T_3, T_5, T_{10}, T_{12}), 'No Growth' (T_1, T_2, T_4, T_8) and 'Slow Decay' ($T_6, T_7, T_9, T_{11}, T_{13}, T_{14}$) - see Chapter 4; (ii) that the Fast Growth and Medium Growth automata from the two-state niches ($2A$ and $2B$) were present in the same proportions as in their original niche composition albeit at a very low concentration representing just 3.3% of the population. The remainder of two-state automata observed in those original exclusively two-state niches had gone extinct in the joint population; and (iii) the continual production of a small subset of automata ($T_{21}, T_{24}, T_{43}, T_{64}, T_{80}, T_{87}$) that were able to survive in the joint population due to their interactions with the one-state automata (in an exclusive two-state population these automaton types would go extinct).

in the joint population. The composition of the surviving population was:

- All nine of the one-state automaton types that were present in niche $1A$ were also present and accounted for 98% of the joint population. The one-state niche ($1A$) had therefore successfully re-generated its identity with a slightly altered structure with the magnitude of difference between these automata accentuated with T_{15} more populous than in the original niche. Examination of the interaction network revealed that in the initial stages of the simulation a total of 25,729 interactions could produce these one-state automata and this accounted mainly for the very fast growth of T_{15}.

- 20 of the 42 automata that represented most of the Fast Growth/Medium Growth category automata from niches $2A/2B$ were present and which, collectively, occupied

1.99% of the joint population. The other 22 automata from those niches had gone extinct and therefore niches $2A$ and $2B$ did not re-generate in a joint population. Only the high performing two-state automata from those niches were able to survive.

- A very low frequency (0.01%) of six two-state automata (T_{21}, T_{24}, T_{43}, T_{64}, T_{80}, T_{87}) that did not belong to any previously observed niches were continually produced in the joint population albeit in very small numbers. Their interactions with the one-state automata enabled their own continual production whereas previously they did not survive in an exclusively two-state population. This may indicate the assimilation of new automata.

The persistence of a small subset of the two-state automata within a space (i.e. the lattice) dominated by a successfully reproduced one-state niche ($1A$) suggested that a form of passive assimilation had occurred in the joint population.

7.4 The dynamics of a joint one-state/two-state population under zero diffusivity conditions

The joint population of one-state and two-state automata was simulated for 10^7 iterations under conditions of zero diffusivity on the lattice ($c = 0, v = 0, \Phi = 0$). The results (see Figure 7.4) showed a strong re-generation of niche $1B$ with T_4 (47%) and T_2 (44%) dominating the niche with the one-state 'boundary' automata T_1 and T_8 also increasing their concentration to collectively occupy 5% of the lattice. The remaining automata consisted of a low frequency of the one-state automata T_3, T_5, T_{10}, T_{12} (3%) and a very low frequency of 12 two-state automata (1%) that were originally the dominant automata in niche $2C$.

The composition of the one-state automata in the population was consistent with niche $1B$ and hence the one-state niche was successfully re-constructed in a competing population of 1,888 automaton types. The surviving two-state automata were those that were operating the 'replicate & lock-in' survival mechanism in niche $2C$ which - although not a superior strategy to the 'protected outgrowth' mechanism of the one-state population - provided a degree of competitiveness. Interestingly, all two-state automata that were operating the 'mutual maintenance' survival mechanism went extinct even though they initially grew in number more rapidly than any other two-state automata in the early stages of the simulation. Their number were depleted as they were replaced by the high performing one-state automata and the 'replicate & lock-in' two-state automata where both groups had used the 'mutual maintenance' automata as a food set.

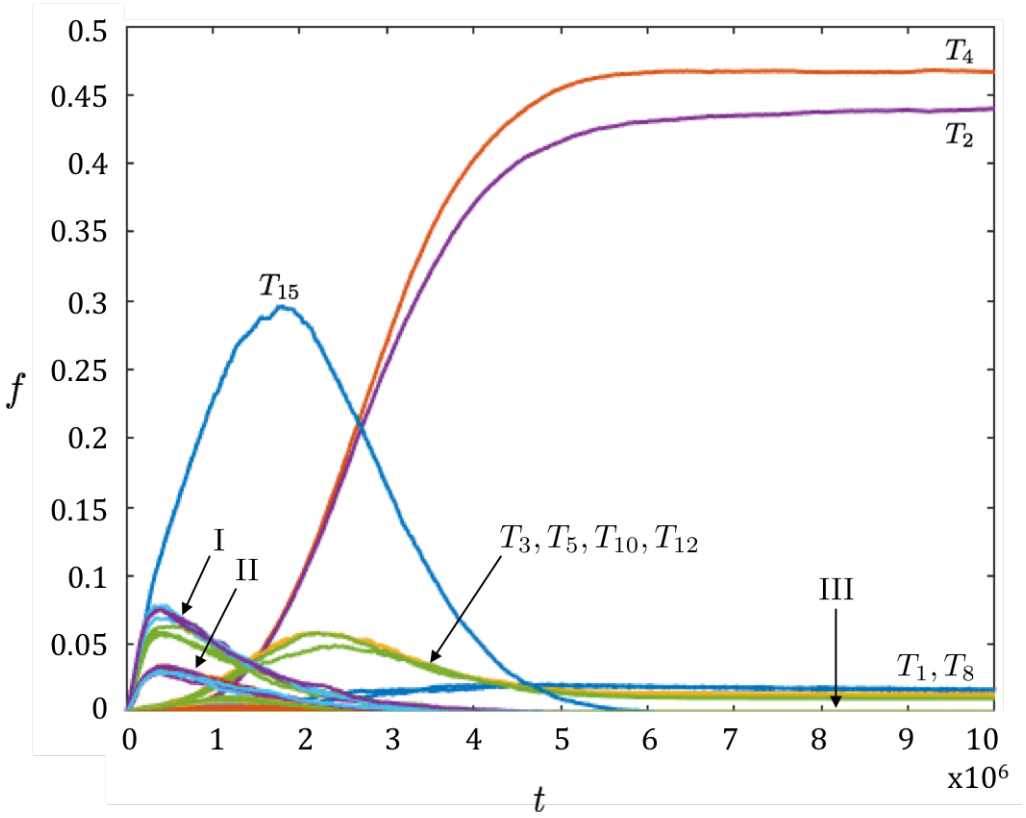


Figure 7.4: The time-series frequency distribution plot for the joint population of one-state and two-state automata under conditions of zero-diffusivity ($c = 0, v = 0, \Phi = 0$). As can be seen the one-state niche $1B$ formed readily (as indicated by the frequency distribution of automata T_1, T_2, T_4, T_8 at $t = 10^7$) and which came to dominate the population. The two-state population followed a similar trajectory to that which formed niche $2C$ however the 'mutual maintenance' automata that grew quickly early in the simulation (I and II) decayed rapidly after $t = 0.5 \times 10^6$ and eventually went extinct leaving only the 'replicate & lock-in' automata (III) which were able to survive in the joint population albeit at a very low frequency.

Examination of the one-state/two-state joint interaction matrix indicated that the 'mutual maintenance' two-state automata produced the one-state automata in the majority of interactions that occurred. As such, and as was the case with the 'replicate & lock-in' two-state automata (see Chapter 5), the one-state automata were using the 'mutual maintenance' automata as a food set in their own production. Given the very rapid growth of one-state automata across the lattice this led to a high intensity consumption of this food set at a rate that did not give the 'mutual maintenance' automata pairs enough time to produce (maintain) each other thus disrupting their survival mechanism. Consequently, they were rapidly depleted from the population. The one-state automata appeared to be little affected by this extinction event. By comparison, the two-state 'replicate & lock-in' automata decayed in number and this was exacerbated as most of the interactions they

had with the dominant one-state automata generated more highly competitive one-state automata. Nevertheless, this group of two-state automata did persist in the population over extensive time periods and this was confirmed with multiple re-runs of the simulation (i.e. multiple simulations were performed and after 10^7 iterations the population was examined and demonstrated the continued presence of these 14 two-state automata albeit at a very low frequency).

At $t = 1$ the production threshold for the joint population was $H(X) = 7.4$ bits, the average structural complexity was $< C_\mu(T) >= 0.93$ bits and the interaction network complexity was $C_\mu(G) = 18.6$ bits. At $t = 10^7$ these were: $H(X) = 4.65$ bits, $C_\mu(T) = 0.78$ bits and $C_\mu(G) = 3.56$ bits. Compared to the equivalent measurements from niche $1B$ and niche $2C$:

niche	$H(X)$ bits	$< C_\mu(T) >$ bits	$C_\mu(G)$ bits
joint	2.8	0.78	3.56
$1B$	2	0	2.6
$2C$	6.29	0.94	8.98

Table 7.1: Comparison of key measurements between the joint population, niche $1B$ and niche $2C$.

As can be seen in Table 7.1 the steady-state joint population under zero-diffusivity conditions had a lower production threshold compared to the two-state niche $2C$ (with a production threshold of $H(X) = 2.8$ bits compared to $H(X) = 6.29$ bits for niche $2C$). The primary reason for this difference were the fewer remaining automata in the joint one-state/two-state population of 36 automaton types compared to the 1,568 surviving automaton types in niche $2C$. For similar reasons the interaction network complexity was also lower in the joint population than niche $2C$ and, indeed, the difference here was accentuated due to the more uniformly spread frequency of automata in niche $2C$ (i.e. a more uniformly spread population increases our uncertainty over which automata will interact in the next time-step). It was clear from examination of the population structure of the joint population compared to niche $2C$ that the former had two highly dominant one-state automata (T_2, T_4) that accounted for nearly 90% of the population. Hence, there was more certainty over which automata were likely to interact in the next time step (as quantified with a lower interaction network complexity measurement). Finally, the steady-state joint population had a lower average structural complexity compared to niche $2C$ due to the presence of one-state automata which have a structural complexity of $C_\mu(T) = 0$ bits thus reducing the population average.

7.5 The dynamics of the one-state automata of niche $1A$ combined with the two-state automata of niche $2B$ under initial uniform conditions

The nine automata from the one-state niche $1A$ and the 21 automata from the two-state niche $2B$ were combined into a single population consisting of 30 one-state/two-state automata[2]. The interaction network for this population was generated $G_{1A,2B}$ and analysis of the network revealed that new interactions had been created between the one-state and two-state automata (see Figure 7.5). Through these new interactions the $1A$ automata were produced from up to 252 interactions and the $2B$ automata from 462 interactions. In their original independent niches there were 63 and 315 interactions respectively and so the automata were benefiting with an additional 189 interactions producing $1A$ automata and an additional 147 interactions producing $2B$ automata as a result of their co-location on the lattice.

A simulation of 90,000 automata interacting under well-mixed conditions was run with the population initially distributed evenly giving a uniform frequency distribution at $t = 1$. The simulation was iterated for 10^7 iterations and the time-series of the frequency distribution (see Figure 7.6) clearly showed that the $1A$ niche automata came to dominate the population from the outset. By comparison, the $2B$ niche automata rapidly decayed to occupy just 1.3% of the population although none went extinct. As such, even though the two-state automata were not competitive under these conditions they did persist. Examination of the interaction network showed that each of the one-state automata had a production advantage over the two-state automata by each being potentially produced from 28 interactions compared to 22 interactions for each of the two-state automata respectively. The persistence of the two-state automata was partly courtesy of their interactions with highly concentrated one-state automata that allowed them to replicate themselves (Figure 7.5 illustrates the mutual production between the two sets of automata). However, the $1A$ niche automata did not re-construct the niche $1A$ structure because each of these automata were produced in equal amounts (from 28 interactions each) and the final order of these automata was due to the stochasticity of the selection of interacting automata (the simulation was repeated a further four times to confirm this observation).

[2]Simulations were re-run using the niche $2A$ automata instead of the niche $2B$ automata. The results were quantitatively and qualitatively very similar.

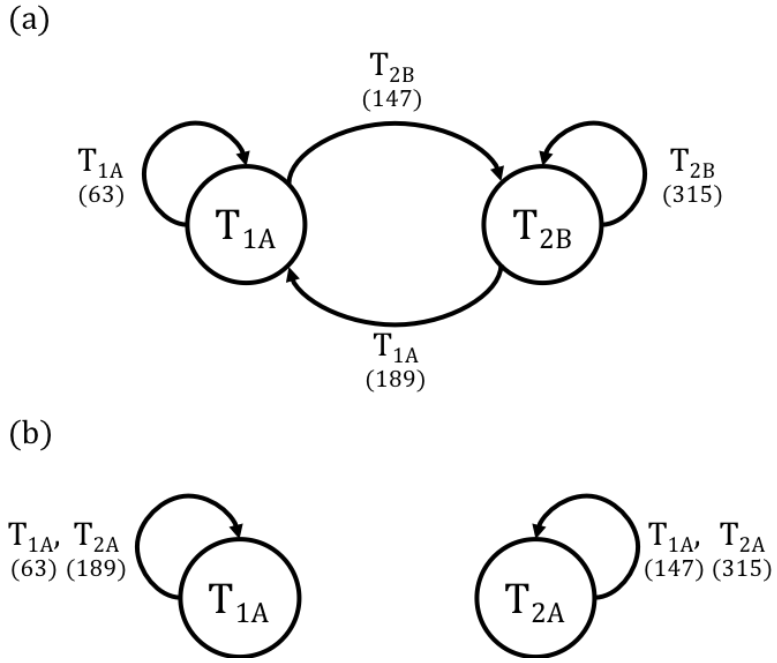


Figure 7.5: The interaction networks for the set of automata from the one-state niche $1A$ (T_{1A}), the two-state niche $2A$ (T_{2A}) and the two-state niche $2B$ (T_{2B}). This diagram captured the $T_b \circ T_a = T_c$ relationship with the direction of the arrow indicating the T_a to T_c relationship which was transformed by the T_b automata as indicated on the edge label: (a) the one-state niche $1A$ and two-state niche $2B$ automata interaction network where 63 interactions ($T_{1A} \circ T_{1A} = T_{1A}$) were the one-state automata reproducing each other, 147 interactions involved T_{1A} and T_{2B} automata that generated all of the T_{2B} automaton types according to $T_{2B} \circ T_{1A} = T_{2B}$, 315 interactions were generated exclusively from two-state automata $T_{2B} \circ T_{2B} = T_{2B}$ that only generated $2B$ automata and 189 interactions whereby the two-state automata interacted with one-state automata to produce one-state automata ($T_{2B} \circ T_{1A} = T_{1A}$); (b) the interaction network of the $1A$ niche and $2A$ niche automata showing a different structure to (a). Here the transformation of the output from T_{1A} automata by a T_{2A} automata produced more T_{1A} automata and, likewise, the transformation of the output from the T_{2A} automata by T_{1A} automata produced T_{2A} automata. Although the topology of interactions networks (a) and (b) were different the population dynamics and steady-state structure of the population were quantitatively and qualitatively very similar.

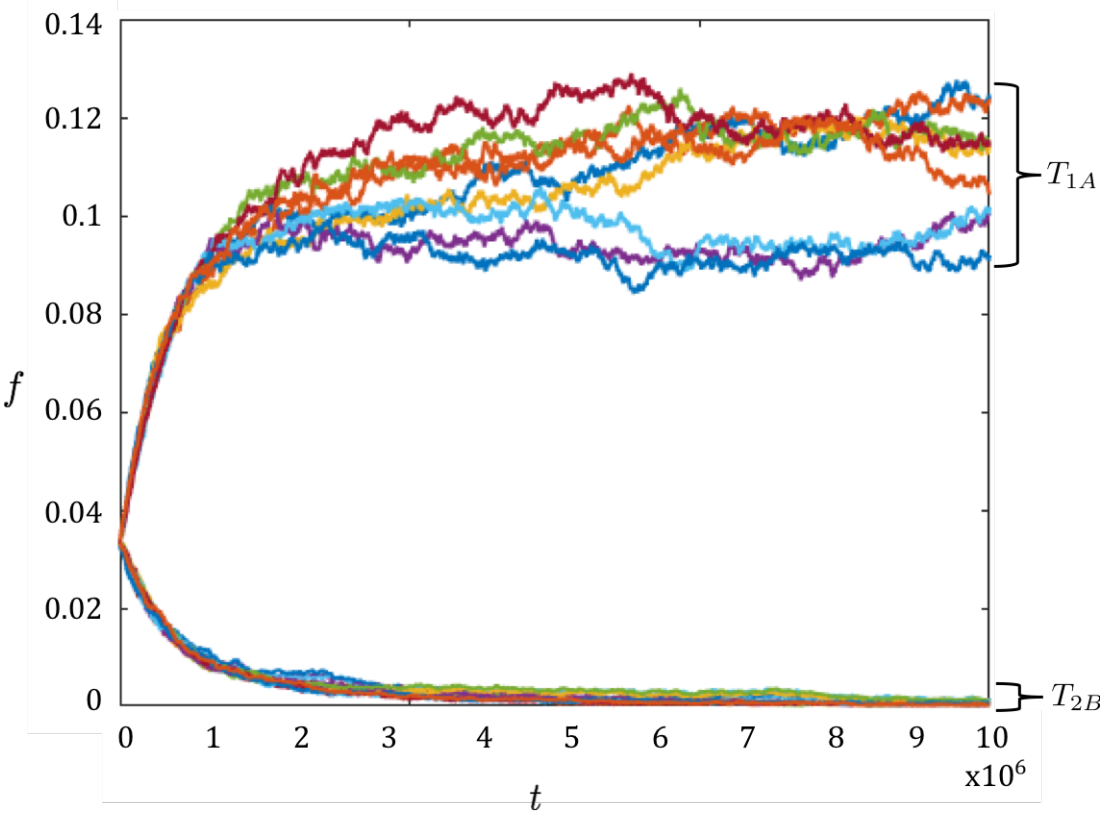


Figure 7.6: The time-series of the frequencies of each automata in the joint population of automata from niche 1*A* and 2*B* distributed evenly at $t = 1$ and evolved under well-mixed conditions ($c = N, v = n, \Phi = 0$) for 10^7 iterations. The one-state automata experienced rapid growth leading to their dominance of the population.

7.6 The dynamics of the one-state automata of niche $1A$ combined with the two-state automata of niche $2B$ initialised to their original niche structure

A joint population was created as per section 7.5 consisting of 30 automaton types: nine automaton types from niche 1*A* and 21 automaton types from niche 2*B*. The initial frequencies of the automata were in proportion to their frequency of occurrence in their original niches. The assumption here was that each niche initially contributed towards 50% of the population and, as such, with a population size of 90,000 each niche was represented by 45,000 automata. Within that allocation the original niche frequency distributions were re-created e.g. the T_{15} automata type occupied 22% of niche 1*A* and, as such, would occupy 22% of the 50% allocated to niche 1*A* giving its initial concentration in the joint population as 11%. Table 7.2 shows the initial frequencies allocated to each of the 30 automaton types

at $t = 1$.

The simulation was run for 10^7 iterations and the resulting population dynamics are shown in Figure 7.7. The initial concentration of automata was proportional to its frequency of occurrence in its original niche composition. As can be seen in Figure 7.7 and Table 7.2 (the final f_i column) the one-state automata grew significantly from constituting 50% of the population at $t = 1$ to 97% of the population at $t = 10^7$ leaving the two-state population to decay to occupy just 3% of the population.

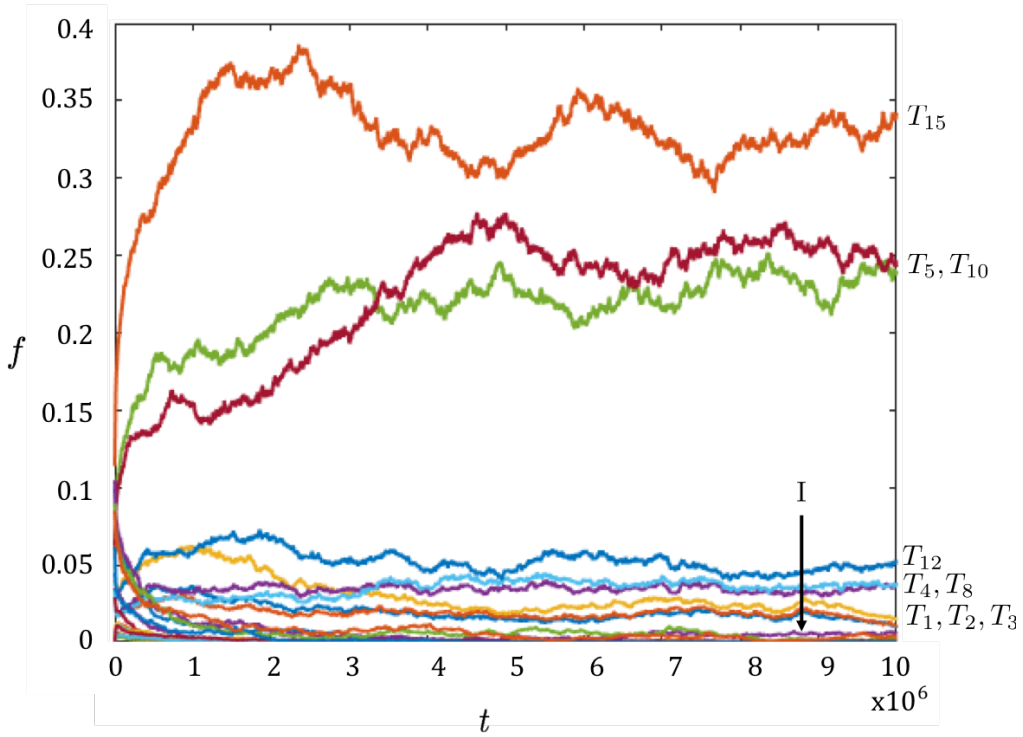


Figure 7.7: Population dynamics of the joint population of automata from niche $1A$ and $2B$ distributed at $t = 1$ according to their proportions in their original niches. The population was evolved under well-mixed conditions ($c, v = 0$ and $\Phi = 0$) for 10^7 iterations. As can be seen the three $1A$ niche automata (T_5, T_{10}, T_{15}) experienced rapid growth and came to dominate the population whilst six $2B$ niche automata went extinct leaving a reduced number of two-state automata (I).

The dominant automata (T_{15}, T_5, T_{10}) benefited from an increase in the number of times that they were produced in a joint $1A$,$2C$ niche population combined with a higher initial frequency relative to the rest of the population[3]. This advantage was quantified by calculating the interaction network complexity ($C_\mu(G_i)$) for each automata type (i) at

[3]The $1A$ niche automata T_3, T_{12} which were as competitive and populous as the T_5, T_{10} in an isolated $1A$ niche environment were not produced as often from interactions with the $2B$ niche automata as T_5, T_{10} and yet were still able to endure in the joint niche population.

	T_i	initial f_i	final f_i	initial f_i - final f_i	$C_\mu(G_i)$
niche 1A	T_1	0.034	0.017	-0.017	2.8
	T_2	0.034	0.024	-0.01	2.8
	T_3	0.07	0.035	-0.035	2.8
	T_4	0.035	0.028	-0.007	2.8
	T_5	0.06	0.17	0.11	4.6
	T_8	0.033	0.038	0.005	2.8
	T_{10}	0.062	0.25	0.188	4.6
	T_{12}	0.062	0.056	-0.006	2.8
	T_{15}	0.11	0.35	0.24	4.6
$\sum_i f_i$		0.5	0.97	0.47	
niche 2B	T_3	0.0001	0	-0.0001	1.6
	T_4	0.0003	0.0001	-0.0002	1.6
	T_{20}	0.00005	0	-0.00005	1.6
	T_{22}	0.0002	0.0005	0.0003	1.6
	T_{36}	0.032	0	-0.032	3.2
	T_{39}	0.1	0.003	-0.097	3.2
	T_{40}	0.0003	0.001	0.0007	1.6
	T_{79}	0.0002	0.0017	0.0015	1.6
	T_{102}	0.11	0.01	-0.1	3.2
	T_{134}	0.0001	0	-0.0001	1.6
	T_{137}	0.0003	0.0001	-0.0002	1.6
	T_{204}	0.0001	0.0005	0.0004	1.6
	T_{207}	0.0001	0.0003	0.0002	1.6
	T_{303}	0.0001	0	-0.0001	1.6
	T_{309}	0.0001	0.0002	0.0001	1.6
	T_{402}	0.05	0	-0.05	3.2
	T_{411}	0.09	0.0016	-0.084	3.2
	T_{555}	0.0001	0.0007	0.0006	1.6
	T_{561}	0.0001	0.0005	0.0004	1.6
	T_{766}	0.04	0.005	-0.035	3.2
	T_{775}	0.08	0.003	-0.077	3.2
$\sum_i f_i$		0.5	0.03	-0.47	

Table 7.2: Comparison of the initial and final frequencies of each automata type in the joint one-state niche (1A) and two-state niche (2B) population. The interaction network complexity $C_\mu(G_i)$ of each automata type is shown. NOTE: the original indices for referencing the niche 2B automata have been used to aid comparison to the results of Chapter 5 and should not be confused with the niche 1A automata with the same index number. The simulation used the indices $i = 1...30$ for each automata with niche 1A automata indexed $i = 1-9$ and the niche 2B automata indexed as $i = 10-30$.

$t = 1$ and the results are shown in the last column of Table 7.2. For the $1A$ niche automata there was an association of a higher $C_\mu(G)$ with better overall performance throughout the simulation e.g. T_5, T_{10}, T_{15} had the highest $C_\mu(G)$ values at 4.6 bits each which was significantly higher than the next lower measurement at 3.2 bits which was measured for seven $2B$ niche automata. A larger number of interactions involving automata that had a higher frequency in the population yielded a higher $C_\mu(G_i)$ value e.g. the total frequency of all automata at $t = 1$ that could interact to produce: T_{15} was 0.86, T_1 was 0.23 and the two-state automata T_{775} was 0.73. As the population reached a steady-state it was interesting to note that the $C_\mu(G_i)$ values for the interaction network of each automata were converging to 2.4 bits. This indicated that the increased order that emerged in the population as it evolved had reduced the uncertainty about which automata will be produced i.e. more structure had emerged in the population. Examination of the interaction network showed that the loss of six two-state automata had reduced the production rate of all automata e.g. one-state automata were produced from 16 interactions rather than 28 initially, and the remaining two-state automata were produced from 11 interactions from 22 initially.

7.7 Disturbance of the one-state niche $1A$ from an influx of two-state niche $2B$ automata

To examine the effect of an inflow of automata from an established two-state niche ($2B$) into an existing one-state niche ($1A$) a series of simulations were run under well-mixed conditions ($c = N, v = n$) with a uni-directional flow of the $2B$ automata into the $1A$ automata niche at various rates in the range $0 < \Phi < 1$. On each iteration of the algorithm either a new automaton was created from interactions within the existing population or from the random replacement of an existing automaton with an automaton selected from niche $2B$. The automata transferred from niche $2B$ was selected probabilistically from the frequency distribution of the $2B$ population and, as such, higher frequency automata were more likely to be selected to be transferred into niche $1A$. It was assumed that the contributing niche $2B$ continually produced automata to maintain its steady-state structure and that the loss of its automata to niche $1A$ was inconsequential (at most, only one automaton would be removed from niche $2B$ on each iteration which would represent a very small fraction of that niche's population). Niche $2B$ automata entering niche $1A$ were able to interact with incumbent automata in the niche and this caused changes to the interaction network in the receiving population. Each two-state automata transferred in

this way replaced an incumbent automata in the receiving niche. Over time this meant that two-state automata that had become part of the receiving niche - either through influx or from endogenous production - were themselves possibly replaced by incoming automata. The simulation was initialised by setting the frequency of the automata in both niches to the proportions that they were present in their original steady-state niches and the simulation was run for 10^7 iterations.

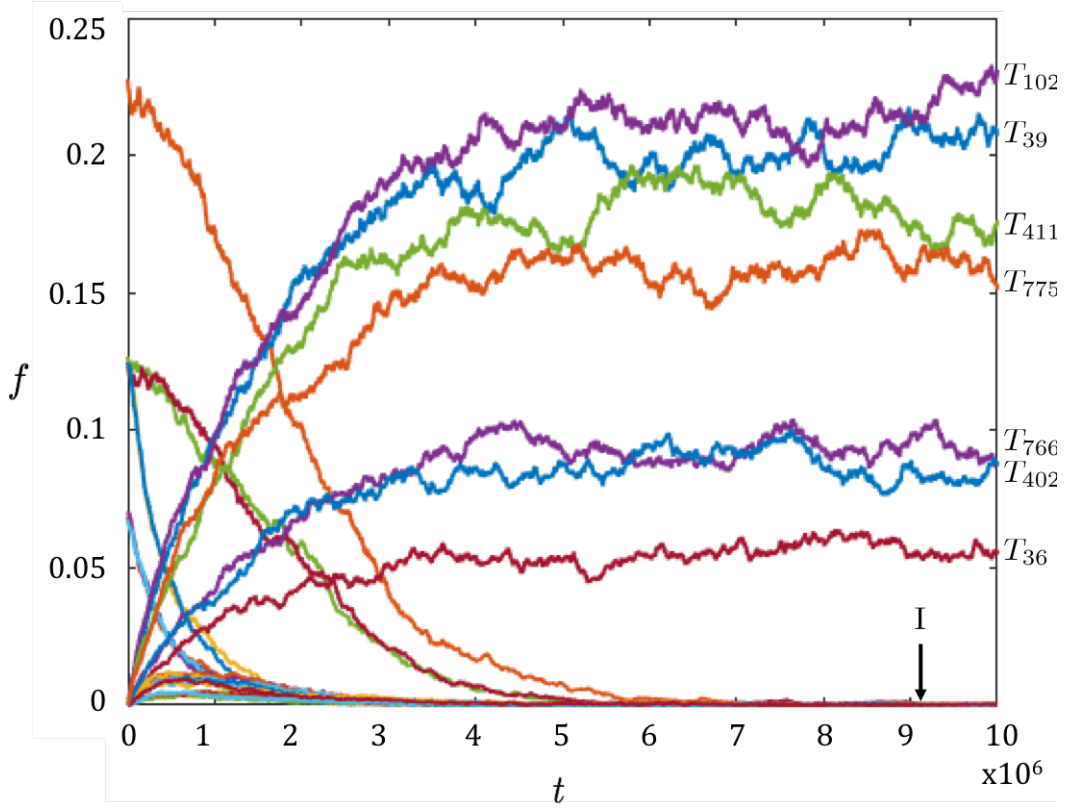


Figure 7.8: Time-series frequency distribution for a simulation of the random replacement of incumbent niche 1*A* automata with two-state automata from niche 2*B* at the rate $\Phi = 0.05$. Selection of automata from niche 2*B* was randomly determined with higher frequency automata in that niche more likely to be selected to replace an incumbent automata. The initial population was exclusively the one-state automata from niche 1*B* ordered in the proportions in which they present in their original niche. As can be seen even with a very low rate of replacement of $\Phi = 0.05$ the two-state niche 2*C* was reproduced in this population to the detriment of the incumbent one-state automata. The automata group labelled as 'I' were the low frequency automata from niche 2*B*.

As can be seen in Figure 7.8 with $\Phi = 0.05$ the structure of niche 2*B* was reproduced entirely in the 1*A* niche with the complete loss of all one-state automata. Examination of the interaction network in the incumbent population showed that the two-state automata were being produced from 462 interactions compared to the 252 interactions that produced

the one-state automata. As the one-state automata went extinct this reduced the number of two-state interactions to 315 interactions however this was in the absence of any competition from the one-state automata. For all values of $0 < \Phi \leq 1$ the two-state niche was reconstructed in the one-state population and came to dominate the population with a subsequent loss and ultimately extinction of the one-state automata. The value of Φ determined how quickly this was realised. In other words, given enough time the interaction network of the two-state niche would be re-constructed in the one-state niche even when the rate of influx was very low (e.g. $\Phi = 0.01$).

7.8 Perturbation of a one-state population via. the influx of two-state automata

The simulation was set-up according to that described in section 7.7 except that the receiving population was now the unstructured one-state population of 15 automaton types and the contributing population was the unstructured two-state population of 1,873 automaton types. Four simulations were each run for 5×10^6 iterations with $\Phi = 0.05, \Phi = 0.5, \Phi = 0.8, \Phi = 0.9$ respectively and the results are shown in Figure 7.9.

Figure 7.9a was the result of a very low rate of influx ($\Phi = 0.05$) where there was a 5% chance of a two-state automata replacing an incumbent automata in the population. There was a slow decay of all incumbent one-state automata (with the exception of T_{15}) as they were replaced by the influx of two-state automata. T_{15} initially underwent fast growth which began to level off towards the end of the simulation. The incoming two-state automata were self-organising with the niche $2A$ and $2B$ automata being produced at a rate faster than new two-state automata were fluxing into the population. This led to a delineation of the $2A, 2B$ automata from other two-state automata as the former were now being produced endogenously to the point where the fast growth automata T_{95} and T_{102} from niches $2A$ and $2B$ respectively outnumbered the previously competitive one-state automata T_3,T_5,T_{10},T_{12}. The very low rate of influx allowed the interaction network to dominate population dynamics.

By comparison, Figures 7.9b-d demonstrated the opposite effect whereby the influx rate was at a rate where the effect of the interaction network was heavily inhibited in driving population dynamics. For example, the two-state automata that were now present in the receiving population did not self-organise into niches $2A, 2B$ but rather stayed as an unstructured sub-population of the one-state population. In Figures 7.9b-c the T_{15} automata were able to continue to be produced 50% and 20% of the time respectively

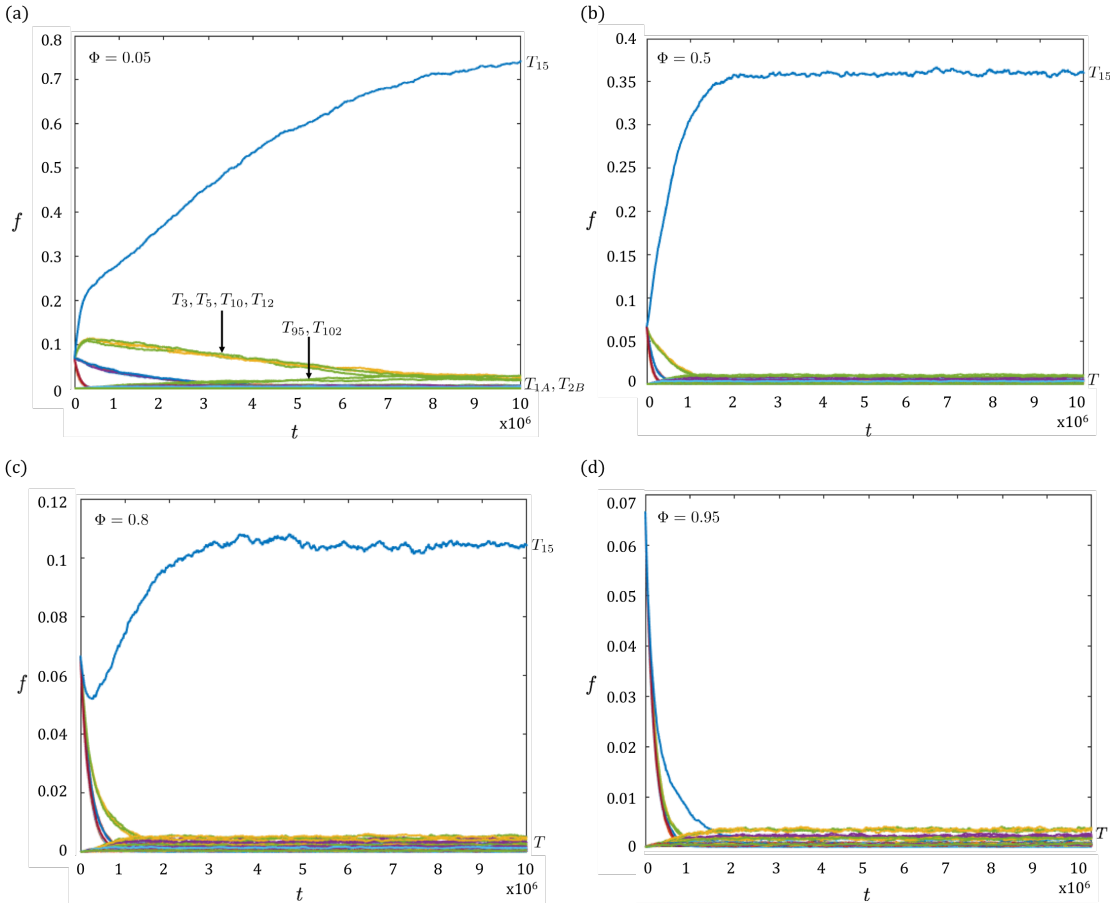


Figure 7.9: The time-series frequency distributions for four simulations of the random replacement of incumbent one-state automata population (15 types) with two-state automata population (1,873 types) for various values of Φ over 10^7 iterations: (a) with $\Phi = 0.05$ the one-state automata T_{15} undergoes rapid and continued growth to dominate the population whilst the remaining one-state undergo a reduction in concentration whilst incoming two-state automata established niches $2A$ and $2B$ concurrently; (b-c) with $\Phi = 0.5$ and $\Phi = 0.8$ respectively the endogenous interactions in the receiving population were disrupted to the point where two-state automata already in that population were unable to reproduce the niches $2A$ or $2B$; (d) with $\Phi = 0.95$ all structure was lost in the receiving population as the replacement of automata was driven from an unstructured two-state population.

and therefore were able to persist under a moderate ($\Phi = 0.5$) to high ($\Phi = 0.8$) influx of two-state automata. However, as shown in Figure 7.9d with an influx rate of $\Phi = 0.95$ all structure was lost as the population dynamics were driven 95% of the time by sampling from an unstructured population of 1,873 two-state automata.

7.8.1 The effect of removing the perturbation

To examine whether the two-state automata arriving in the one-state population were being 'assimilated' or 'accommodated' four simulations were run that examined the effect of switching off the influx ($\Phi = 0$) of two-state automata into the one-state population from $t = 2 \times 10^6$ and, in two simulations, re-enabling the influx but at a reduced rate ($\Phi = 0.65$) from $t = 3.5 \times 10^6$. The results of these four simulations are shown in Figure 7.10.

Figure 7.10a shows that the one-state automata underwent a steady decline in concentration in the presence of an influx of two-state automata at the high rate of $\Phi = 0.85$ and this led to the extinction of all one-state automata except T_{15}. Once the influx of two-state automata had been disabled ($\Phi = 0$) at $t = 2 \times 10^6$ then the one-state T_{15} automata very quickly dominated the population. This was because the interactions between the two-state automata produced the T_{15} automata more often than they did each other. As T_{15} grew in concentration it was selected more and more frequently to interact with itself to create the self-replication interaction $T_{15} \circ T_{15} = T_{15}$ to reproduce itself. The decrease in the rate at which T_{15} came to dominate the population was due to the process of selecting an automaton to remove from the population which, due to the method used, meant that the greater the concentration of an automata the more likely it was to be selected for removal from the population. Given the stochastic nature of the interaction and removal process this meant that on some iterations non-T_{15} automata were removed as shown by the gradual decline of the remaining automaton types. Incidentally, the remaining automata were primarily the niche $2A$ and $2B$ automata which continued to persist throughout the simulation. The population dynamics from $t = 2 \times 10^6$ and with $\Phi = 0$ were driven entirely by the interaction network which enabled the self-producing networks of this population to emerge to form a steady state population structure characterised by the dominance of T_{15}. This population had adapted to the two-state automata as they were now able to continually produce themselves independently of a steady influx of their type from outside i.e. the 'operational limits' [16] of this autopoietic system was entirely enclosed within the population and was not dependent on any external processes. Figure 7.10c shows the results of running a similar simulation that re-introduced an influx of two-state automata (at a rate $\Phi = 0.65$) at the 3.5×10^6 iteration which led to the reduction in concentration of T_{15} and the niche $2A, 2B$ automata as the production of new automata was disrupted by the influx of two-state automata.

Figure 7.10b shows the one-state automata decaying quickly due to the very high influx rate ($\Phi = 0.95$) of two-state automata into the population to the extent that they go extinct. This was evident once the influx rate was disabled ($\Phi = 0$) at $t = 2 \times 10^6$ and the

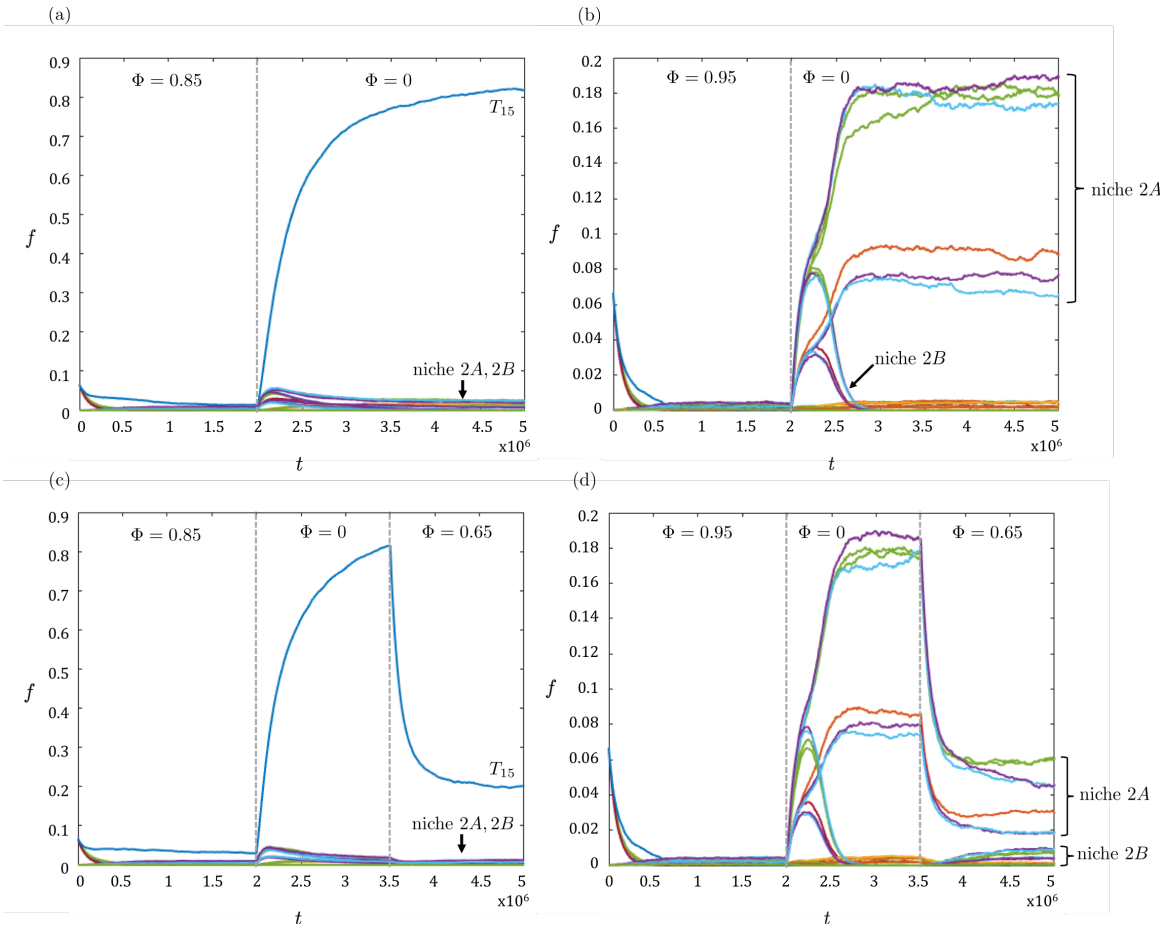


Figure 7.10: The time-series frequency distributions for four simulations where (a) from $t = 1$ the influx of two-state automata was at the rate $\Phi = 0.85$ and was then halted ($\Phi = 0$) at the $t = 2 \times 10^6$ iteration for the remainder of the simulation showing the rapid growth of the T_{15} one-state automata and the presence of the two-state automata from niche $2A$ and $2B$; (b) from $t = 1$ the influx of two-state automata was at the more aggressive rate of $\Phi = 0.95$ leading to the extinction of all one-state automata by the 2^6 iteration at which point the influx of automata was halted ($\Phi = 0$) for the remainder of the simulation leading to the reproduction and competition between niches $2A$ and $2B$ until a divergence event at the 2.25×10^6 iteration leading to the domination of the population by the niche $2A$ automata; (c) the same settings and timings were used as per (a) except at the 3.5×10^6 iteration the influx of two-state automata was re-enabled at a lower rate of $\Phi = 0.65$ for the remainder of the simulation showing a significant reduction in the concentration of T_{15} until a new steady-state was reached; and (d) the same settings and timings were used as per (b) except that at the 3.5×10^6 iteration the influx of two-state automata was re-enabled at $\Phi = 0.65$ which led to the reduction in concentration of the niche $2A$ automata and an increase in the concentration of niche $2B$ automata.

two-state automata completely dominated the population and re-created the competitive dynamics seen with the formation of niche $2A$ after a period of competition with the niche $2B$ automata (see Chapter 5). Figure 7.10d shows the effect of re-introducing an influx of two-state automata (at a rate $\Phi = 0.65$) which, predictably, disrupts the internal production

dynamics to reduce the concentration of the niche $2A$ automata whilst increasing the concentration of the niche $2B$ automata. The effect of an external perturbation on two-state automata production dynamics was discussed in Chapter 5 and was seen again here with the neutralisation of the competition between those two niches to the extent that they could co-habit the population.

The rate of $\Phi = 0.65$ was determined[4] to be the maximum rate at which a population structure was retained. With $\Phi > 0.65$ the population structure collapsed due to a significant interruption of the internal production dynamics caused by the high rate of influx of two-state automata.

These simulations demonstrated how 'fragments' of two-state automata networks could re-build the network required to reproduce a two-state niche via. the accommodation of two-state automata into an initially one-state population. This supports Maturana's proposed mechanism by which autopoietic systems reproduce [7].

These simulation results also revealed an interesting sequence of phases (see Figure 7.11) that the population went through beginning with the destruction of the incumbent population via. the rapid assimilation of foreign automata (at a rate $\Phi = 0.95$) through to the establishment of internal production dynamics (with an impermeable boundary with $\Phi = 0$) to continually produce those foreign automata which become the incumbent automata to form either niche $2A$ or $2B$ even in the presence of a re-established influx of two-state automata at a lower rate of $\Phi = 0.65$.

In a chemical or biological setting this would imply that a foreign material that had successfully entered into an interior space and displaced the incumbent entities, would need to somehow spontaneously form and regulate its systems interface to prevent the continued flow of foreign material into its recently claimed space (i.e. establishing $\Phi = 0$). This would be necessary to allow the relationships between the now encapsulated entities to form a network of interactions leading to their self-production and the emergence of a steady-state organisation. This would constitute the reproduction of an external niche within a new space. Once established this niche would 're-enable' its systems interface sufficiently to allow a regulated flow (e.g. in these simulations the maximum rate was $\Phi = 0.65$) of foreign material that was sufficient to allow it to structurally couple to its environment. These simulations have demonstrated the essence of the concept of an autopoietic system as able to self-produce and re-produce from 'fragments' of their production networks [7].

[4]Additional simulations were run in the range $\Phi = 0.5 \rightarrow 0.9$ to isolate the approximate value for $\Phi = 0.65$ as the maximum rate for a niche structure to maintain itself in the presence of an influx of externally generated automata.

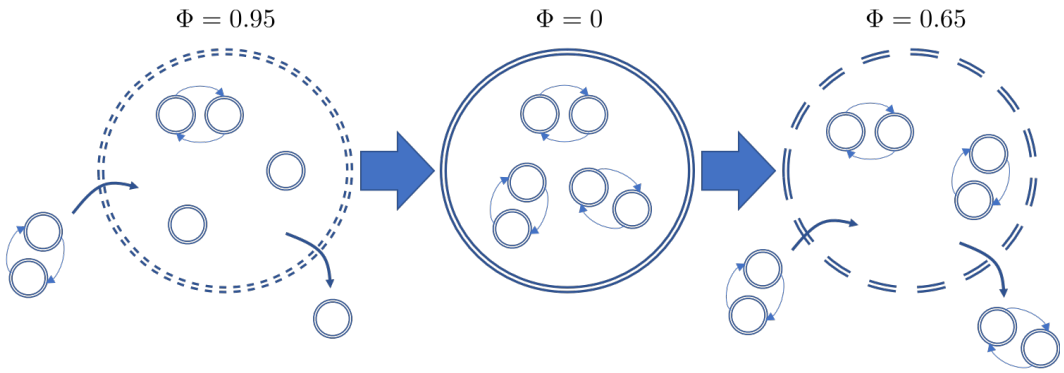


Figure 7.11: With $\Phi = 0.95$ two-state automata entered the one-state population which displaced primarily one-state automata which were removed from the population. At such a high rate of influx all one-state automata were depleted from the population to leave two-state automata remaining. With $\Phi = 0$ the internal production dynamics dominated and this led to the formation of either niche $2A$ or $2B$. With an influx of two-state automata re-established at the rate $\Phi = 0.65$ there was an inflow and outflow of two-state automata however the niche structure was now maintained. In this illustration the boundary lines of each 'cell' signify the rate of influx of automata with solid double lines indicating an impermeable boundary ($\Phi = 0$), large dashed lines indicating a semi-permeable boundary ($\Phi = 0.65$) and small dashed lines indicating a highly permeable boundary ($\Phi = 0.95$).

7.9 Summary

This chapter has investigated whether one-state and two-state populations can maintain and/or reproduce information niches that previously emerged in exclusively one-state or two-state populations (see Chapters 4 and 5 respectively). Three scenarios were simulated: a joint population of 1,888 one-state and two-state automata, a small population consisting of only those automata that constituted the niches $1A$ and $2B$, and the one-state population (and, separately, in its evolved form as niche $1A$) as an incumbent population perturbed by a uni-directional flow of two-state automata replacing the incumbent automata at various rates of $0 < \Phi \leq 1$.

The following simulation results were presented and discussed:

- A joint one-state/two-state population consisting of 1,888 unique automaton types interacting over 10^6 iterations under well-mixed conditions ($c = N, v = n, \Phi = 0$) demonstrated that niche $1A$ emerged and persisted within the joint population. Only the high-growth/medium-growth automata from niches $2A$ and $2B$ were able to persist in the joint population at a very low frequency. Indeed, the one-state niche $1A$ dominated and occupied 97% of the population with the two-state automata occupying the remaining 3.3%.

- A joint one-state/two-state population consisting of 1,888 unique automaton types

interacting over 10^6 iterations under zero-diffusivity conditions ($c = 0, v = 0, \Phi = 0$) demonstrated that niche $1B$ emerged and dominated the population. Niche $2C$ did not emerge although the dominant automata from that niche - the 'replicate & lock-in' automata - did persist at a very low frequency. The 'mutual maintenance' two-state automata from niche $2C$ did not survive and went extinct.

- A joint population consisting of the niche $1A$ automata and the niche $2B$ automata set to an initially equal concentration interacting over 10^7 iterations under well-mixed conditions demonstrated that the $1A$ automata dominated. However, there was no discernible structure to the one-state automata that matched the structure of niche $1A$ whereas the two-state automata - although of a very low frequency - were proportioned in accordance with niche $2B$. The dominance of the one-state automata was due to the additional interactions that produced them from the presence of the two-state automata.

- A joint population consisting of the niche $1A$ automata and the niche $2B$ automata set to an initial frequency distribution that represented their proportions in their original niche configurations. This population interacted over 10^7 iterations under well-mixed conditions. The one-state automata experienced growth at various rates in the early stages of the simulation whilst the two-state automata decayed rapidly. The original niche structures were not maintained.

- A one-state automata population of 15 different types perturbed by two-state automata of 1,873 automaton types replacing incumbent one-state automata at the rates $\Phi = 0.05, \Phi = 0.5, \Phi = 0.8, \Phi = 0.95$ respectively. The one-state automata T_{15} proved to be very robust and a very high rate ($\Phi = 0.95$) of incoming two-state automata was required before it succumbed and eventually went extinct. All other one-state automata went extinct in the presence of any disturbance of two-state automata. Further simulations were run to examine the effect of disabling the influx of automata (i.e. $\Phi = 0$) after 2×10^6 iterations and in the case where all one-state automata had gone extinct by this time (as was the case where $\Phi = 0.95$) this led to the formation of niche $2A$ or $2B$. However, where the one-state automata T_{15} was still present at this time (as was the case where $0 < \Phi \leq 0.8$ up to 2×10^6) this led to it dominating the population. Re-enabling the influx of two-state automata (at a maximum rate of $\Phi = 0.65$) led to these population structures maintaining themselves; with $\Phi > 0.65$ the influx of two-state automata disrupted endogenous production to the extent that any population structure was destroyed.

Analysis of the above results led to the following observations:

- A uni-directional flow of automata from one niche to another led to the reproduction of the structure of the donating population in the receiving population; the velocity with which this reproduction was achieved increased as the influx flow rate increased to a maximum of $\Phi = 1$

- The co-location of one-state and two-state automata did not affect the ability for one-state automata to evolve to the steady-state niche $1A$ under well-mixed conditions. However, the actual structure of the niche was different e.g. the one-state niche was characterised by a very high frequency of T_{15} and a significantly lower frequency of the other one-state automata when compared to the original niche $1A$. Nevertheless, the ordering and therefore the identity of the niche was reproduced.

- An injection of two-state automata drawn from an established niche ($2B$) of 21 automata was far more effective in reproducing itself than two-state automata drawn from a uniform, unstructured ensemble of 1,873 two-state automaton types. This indicated that an efficient, optimised group of automata (as per the $2B$ niche automata) were able to reproduce their own steady-state structure at a far faster rate across a wider range of conditions (where the rate at which this happened was in the range $0 < \Phi \leq 1$ then niche $2B$ would be reproduced). By comparison, an unstructured population of two-state automata required a specific change in conditions (i.e. the disabling of an influx of two-state automata at $t = 2 \times 10^6$ and $\Phi = 0$) before a structure could emerge. Within 2×10^6 iterations of the simulation a two-state population would be assimilated within a one-state population with the subsequent effect on the receiving population determined by the rate at which incumbent automata had been replaced by external two-state automata: (a) with $0 < \Phi < 0.95$ the incoming two-state automata were able to establish their own production dynamics albeit at a very low concentration with the T_{15} one-state automata still present in the population thus demonstrating that the foreign two-state automata had been accommodated in a one-state population; and (b) with $0.95 \leq \Phi \leq 1$ the one-state population had been eliminated leading to the complete dominance and reproduction of the external, unstructured two-state population. However, for this two-state population to form a more ordered structure required the removal of any influx from the external two-state population. From there, the maintenance of the ordinary population dynamics of a two-state population under well-mixed conditions (see Chapter 5) were possible. This

was a demonstrable example of the importance of the 'operational closure' concept of an autopoietic system [16].

- The less structured and diverse that the population of automata that was acting as the source for perturbing and replacing incumbent automata was the more likely it was that the incumbent population would persist. Conversely, the more structured and efficient the source of automata then the less likely the incumbent population would be able to compete and persist. Hence, in a more general chemical or biological setting the nature of and maturity of neighbouring cells or systems should play a contingent role on the viability of an autopoietic system that was exchanging material with its external environment.

- All simulation results exhibited the *active* assimilation of two-state automata alongside, or into, a one-state population that led to changes in the internal structure of that population. This was due to the interactivity that existed between the one-state and two-state automata. The *passive* form of assimilation would only be present where there was no interaction between automata however this would only occur in extremely simple (and therefore trivial) populations e.g. where the range of the incumbent population of automata did not match the domain of any of the incoming automata, and vice versa[5]. Given the assumption that these subsets of automata are self-producing and maintaining means that such mutual exclusion (or disjoint automata sets) were only possible where both sets of automata consisted of just one self-replicating automata each e.g. the T_1 and T_8 one state automata where their respective domain and range of information processing are disjoint.

This chapter has examined the cognition process of autopoiesis through simulating the influx and presence of foreign molecules into unstructured or evolved populations. The next chapter examines cognition as the internal and external flows of information within a self-producing population and with its environment.

[5]As a general notion this means that one set of automata can only ever process say the '0' symbol and the other set of automata can only ever process the '1' symbol.

CHAPTER 8

RESULTS V - ONE-STATE COMPUTATION NICHE SIMULATIONS

8.1 Introduction

This chapter presents the results of simulating a one-state automata population evolving in the computation niche model. The three components that constituted the computation niche model were an environment, a membrane, and an internal replicating population. The membrane was a network of automata that transmitted and received binary information across its own network and exchanged information with the external environment. Conceptually, the membrane separated the internal interacting population (e.g. an information niche) from the environment.

To identify the possible steady-states that the population could reach a wide range of environment settings were simulated. The computation niche model allowed for a wide range of environmental settings to be simulated: (i) the transmission of environmental information *into* the niche (random, a constant '0', or a constant '1'), (ii) the intensity with which that information was transmitted was given by Φ_{in} across the range $0 \leq \Phi_{in} \leq 1$ increasing in 0.1 increments to give 11 different values for Φ_{in}, (iii) the transmission of information *from* the niche into the environment and (iv) the intensity with which niche information was transmitted into the environment was given by Φ_{out} across the range $0 \leq \Phi_{out} \leq 1$ increasing in increments of 0.1 to give 11 different values for Φ_{out}. Two approaches were taken to simulate the computation niche model using these parameters.

The first approach was to run a small number of simulations for different parameter values that represented no noise ($\Phi_{in} = 0$), low noise ($\Phi_{in} = 0.25$), medium noise ($\Phi_{in} = 0.5$)

and high levels of noise ($\Phi_{in} = 0.75$). The aim was to understand, broadly, what the effect of different rates of environmental noise had on membrane activity and, subsequently, the different steady states that the population could reach.

The second approach was a more detailed exploration of other possible steady-states of the population by examining smaller changes in the parameter values. A set of 11 simulations were run for different values of the rate of environmental noise (Φ_{in}) being received into the membrane. In addition, to continue to explore the possible steady states that the niche could reach, another set of simulations were run for 11 different types of environmental information (E) being received into the membrane at 11 different rates (Φ_{in}) which required a further 121 simulations. Hence, a total of 136 simulations were run to explore the possible states that the population could reach under the influence of environmental noise.

A similar approach was taken to examine the effect of emissions from the niche that modulated environmental information. Firstly, the effect of the niche emissions on the environment were examined for four different emission rates ($\Phi_{out} = 0$,$\Phi_{out} = 0.25$,$\Phi_{out} = 0.5$,$\Phi_{out} = 0.75$). Secondly, more detailed simulations were run to examine the effect of different degrees of coupling between the niche and the environment for 11 values of Φ_{in} and 11 values of Φ_{out} that required a total of 121 simulations. In total, 125 simulations were run to explore the possible states that the population could reach where emissions from the niche could modulate environmental noise.

As such, to sufficiently explore all possible steady states of the computation niche under the influence of environmental noise - both modulated and unmodulated - required a total of 261 simulations. The following sections describe the results of these simulations:

- Four simulations to examine the effect of environmental noise on the membrane, with any subsequent effect on the internal self-producing population, under the following conditions: no environment ($E = \emptyset$), a random environment ($E = P(e = 0, e = 1) = [0.5, 0.5]$), a constant 0 environment ($E = P(e = 0, e = 1) = [1, 0]$), and a constant 1 environment ($E = P(e = 0, e = 1) = [0, 1]$). See Section 8.3.

- 11 simulations of the computation niche under the influence of fixed environmental noise proceeding in 0.1 increments ($E = \{[0, 1], [0.1, 0.9], ..., [0.9, 0.1], [1, 0]\}$). See Section 8.3.5.

- 121 simulations of the computation niche under the influence of random environmental noise that increased in intensity in 0.1 increments ($\Phi_{in} = [0, 0.1, ..., 0.9, 1)$ repeated

for each of the 11 environmental settings (($E = \{[0,1],[0.1,0.9],...,[0.9,0.1],[1,0]\}$). See Section 8.3.6.

- Four simulations of the niche coupled to the environment with coupling strength increasing in 0.25 increments from $\Phi_{out} = \{0, 0.25, 0.5, 0.75\}$.
- 121 simulations of the computation niche in the presence of both environmental noise and niche emissions, with values in the range $0 \leq \Phi_{in} \leq 1$ (environment) and $0 \leq \Phi_{out} \leq 1$ (niche), that were increased in 0.1 increments. See Section 8.3.7.

8.2 Set up of the Computation Niche membrane

To examine the effect of a membrane on the production dynamics of a self-producing population a membrane network (M) was initialised consisting of 15 one-state automaton types. The membrane network consisted of 15 vertices and a total of 207 edges (see Figure 8.1). The weightings (λ) on each edge were initialised to the normalised frequencies of the uniform distribution of the population at $t = 0$ e.g. in a 15 automata population the concentration of each automata type was 1/15th. Therefore, at $t = 0$ each edge in the membrane network was equally weighted at $\lambda = 0.0048$. The initial cumulative weightings of the communication channels received by each membrane automaton (M_i) - relative to all other automata in the membrane - is shown in Table 8.1.

M_i	in-degree (k_{in})	out-degree (k_{out})	$\sum \lambda_i$ at $t = 0$	$\sum \lambda_i$ at t_{max} with $E = \emptyset$	$\sum \lambda_i$ at t_{max} with $E = [0.5, 0.5]$
M_1	12	12	0.058	0.056	0.057
M_2	12	12	0.058	0.056	0.057
M_3	12	15	0.058	0.056	0.057
M_4	12	12	0.058	0.056	0.057
M_5	15	12	0.0725	0.074	0.073
M_6	15	15	0.0725	0.074	0.073
M_7	15	15	0.0725	0.074	0.073
M_8	12	12	0.058	0.056	0.057
M_9	15	15	0.0725	0.074	0.073
M_{10}	15	12	0.0725	0.074	0.073
M_{11}	15	15	0.0725	0.074	0.073
M_{12}	12	15	0.058	0.056	0.057
M_{13}	15	15	0.0725	0.074	0.073
M_{14}	15	15	0.0725	0.074	0.073
M_{15}	15	15	0.0725	0.074	0.073
Total	207	207	1	1	1

Table 8.1: The cumulative weightings of the incoming edges for each target membrane automata (M_i) comparing the initial weightings ($t = 0$) with the final weightings ($t = t_{max}$) with and without environmental noise present ($E = \emptyset$ and $E = [0.5, 0.5]$ respectively). The final cumulative weightings of each membrane automaton's incoming edges under those two environmental settings were different from each other and the initial values. This demonstrated how the membrane adapted to reflect the changing structure of the internal self-producing population.

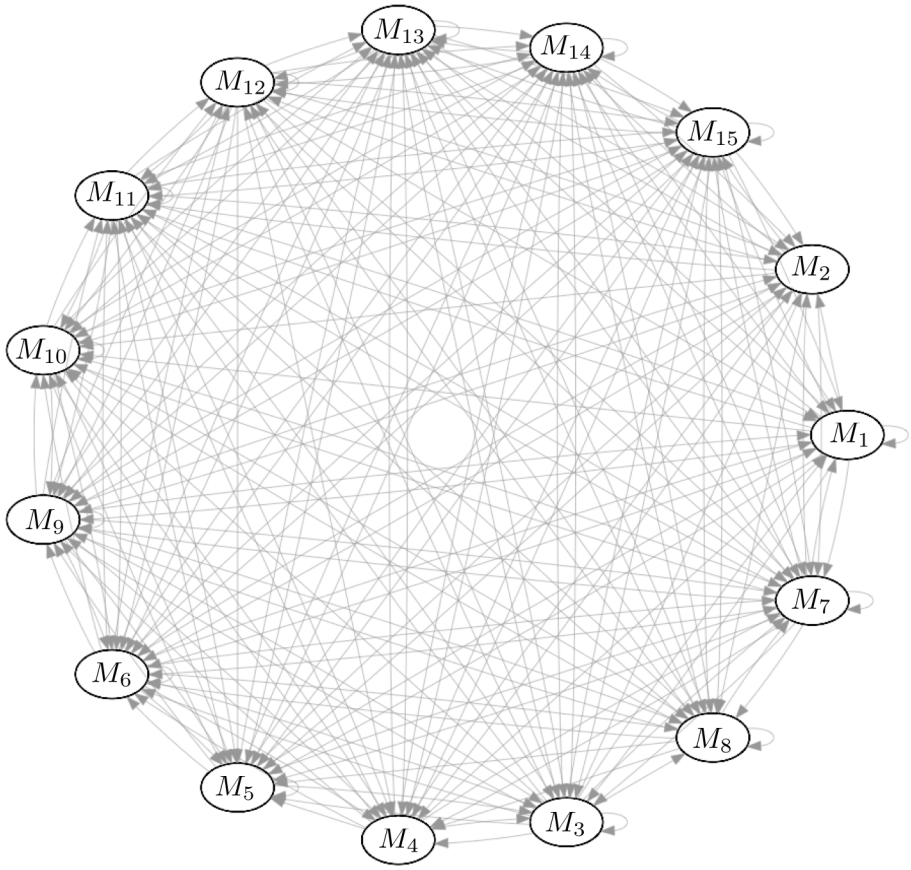


Figure 8.1: The topology of the membrane automata network where the directed edges indicate the flow of transfer of information between the source automata (M_a) to target (M_b) automata from the interaction relationship $T_b \circ T_a = T_c$ i.e. automata M_a emitted information which was received by M_b that then subsequently processed that information according to its internal structure. This was a highly connected network with an average in-degree of 13.8 and an average out-degree of 13.8 giving a 1:1 ratio that indicated a highly symmetrical structure of 207 edges. As each membrane automaton was highly connected this created competition within the membrane network in the form of multiple source automata interfering in each others attempts to influence the activation of shared target automata.

At $t = 0$ the membrane automata had not yet received an input and, as such, they were all set to spontaneously emit their nominal output as given by their internal structure. Where an automaton had the possibility of emitting a '0' or a '1' then the output was chosen with equal probability. The probabilities - as shown in Table 8.2 - were always the same value at $t = 0$ for successive simulation runs when there was no environmental noise[1].

Table 8.2 shows the probabilities of each membrane automata receiving (X) and emit-

[1]With environmental noise present then this had the effect of modulating the information received (X) at each receiving membrane automaton and therefore the probabilities would be dependent on the value of the environmental noise.

	Outgoing Edges		Incoming Edges				
automata	$P(y_i = 0)$	$P(y_i = 1)$	$P(x_i = 0)$	$P(x_i = 1)$	Accepts 0	Accepts 1	P_{max}^{active}
M_1	1	0	0.625	0.375	y	n	0.625
M_2	0	1	0.625	0.375	y	n	0.625
M_3	0.5	0.5	0.625	0.375	y	n	0.625
M_4	1	0	0.375	0.625	n	y	0.625
M_5	1	0	0.5	0.5	y	y	0.5
M_6	0.5	0.5	0.5	0.5	y	y	0.5
M_7	0.67	0.33	0.5	0.5	y	y	0.5
M_8	0	1	0.375	0.625	n	y	0.625
M_9	0.5	0.5	0.5	0.5	y	y	0.5
M_{10}	0	1	0.5	0.5	y	y	0.5
M_{11}	0.33	0.67	0.5	0.5	y	y	0.5
M_{12}	0.5	0.5	0.375	0.625	n	y	0.625
M_{13}	0.67	0.33	0.5	0.5	y	y	0.5
M_{14}	0.33	0.67	0.5	0.5	y	y	0.5
M_{15}	0.5	0.5	0.5	0.5	y	y	0.5

Table 8.2: The information processing behaviour of membrane automata showing the probability of an automata emitting ($P(Y)$) a symbol '0' or '1', the probability of an automata receiving ($P(X)$) a '0' or a '1' and the probability of the activation threshold (P_{max}^{active}) being surpassed to activate a membrane automata.

ting (Y) binary information in the absence of environmental information. Incoming edges (X) to membrane automata could carry symbols that were outside of its domain. This was because some transmitting automata had an output range that surpassed that of the domain of the receiving automata e.g. dual output automata could emit a '0' or '1' at different time-steps whilst mono input automata could only ever process a '0' or '1' but not both. Subsequently, mono input channel automata ignored (i.e. did not process) information that was outside of their domain. The event of triggering a membrane automaton was independent for each input symbol, and as such, the input probabilities X_i were not additive e.g. the T_6 automaton could accept both '0' and '1' symbols but could only execute a transition based on one of those inputs. The input that surpassed the activation threshold of the automaton was chosen as the transition. The probability of an automaton activating at time t was the maximum probability of one of its inputs. Examination of the membrane network determined the nominal P_{max}^{active} value for each automaton which took into consideration the probability of mono input automata receiving out-of-range information from dual output automata.

Figure 8.2 illustrates how the input probability distribution ($P(M_i)$) was calculated for a membrane automaton. As can be seen the cumulative inputs from each incoming edge was normalised to give a two-element probability distribution. This distribution

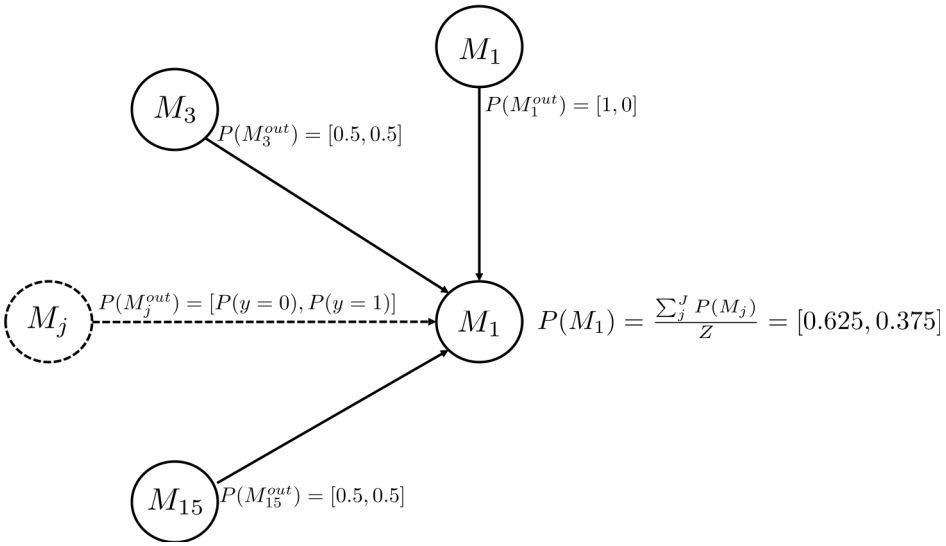


Figure 8.2: An illustrated example of the calculation of P_{max}^{active} for the membrane automaton M_1. Each membrane automata M_j in the set $M_J = \{M_1, M_3, ..., M_{15}\}$ transmitted information to M_1 (it also transmitted to itself) in the form of a two-element probability distribution $P(M_j) = [P(y = 0), P(y = 1)] = 1$. The input function $P(M_1)$ was the cumulative probability distribution of all inputs. In this example the weightings on each edge were assumed to be equal and therefore $P_{max}^{active} = max(P(M_1)) = 0.625$. Under changing conditions the edge weightings modulated the information received by M_1, that could lead to fluctuating values of P_{max}^{active} which subsequently effected the activation behaviour of the receiving automata. Z was a normalising factor.

captured the information that had been collected at the membrane automaton's inputs. To determine whether the membrane activated required this input probability distribution (X) to be filtered to the information processing domain of the receiving automaton (τ) (as per equation 3.8) to give $X' = [0.625, 0.375] \times [1, 0]^T = [0.625, 0]$ where ^{T} was the transpose of the vector τ. As such at $t = 1$ there was a 62.5% chance that the membrane automaton M_1 would activate.

8.3 The effect of a membrane on a self-producing population

Simulations of the computation niche model were run for 1×10^5 iterations[2] with the membrane network initialised as described in section 8.2 and the internal population

[2] The computation niche model performed a synchronous update of the internal population, compared to an asynchronous update which was used in the information niche model, and this required significantly less iterations to generate a steady-state population. The decision to use a synchronous approach was based on the need to ensure that each distributed function (e.g. a membrane automaton or a population-based automaton) was processing the same up-to-date information at the same time.

initialised to a uniform distribution of 90,000 automata across the 15 different one-state automaton types operating under well-mixed conditions.

Four environmental settings were simulated: (a) with no environmental noise ($\Phi_{in} = 0$) meaning that information flow over the membrane were effected only by the membrane itself and changes in population structure, (b) the environment randomly generated 0's and 1's from a uniform probability distribution, (c) the environment only generated the symbol '0', and (d) the environment only generated the symbol '1'. For one simulation setting the environment aperture Φ was set to $\Phi = 0$ indicating that membrane automata activity was determined solely from information received from other membrane automata. For the remaining three simulation settings the environment aperture Φ was set to $\Phi = 1$ which meant that the calculation to determine whether a membrane automata was activated was determined solely by the information it received from the environment. A more in-depth examination of various values for the environmental aperture were also examined (see section 8.8). Sections 8.3.1-8.3.3 interpret the results of the population dynamics shown in Figure 8.3.

8.3.1 The effect of a membrane on production dynamics in the absence of environmental noise

A computation niche consisting of 90,000 one-state population automata and 15 one-state membrane automata were simulated for 1×10^5 with $\Phi_{in} = 0$. Figure 8.3a shows the results of simulating the computation niche in the absence of environmental noise. The processing in the membrane network and the production of new automata were determined entirely by the flow of information (i) within the membrane network, (ii) from the membrane to the internal population, and (iii) changes in population structure reflected in the weightings of the membrane network edges. The simulation was run for 1×10^5 iterations and the results showed that the internal population had evolved to a steady-state structure characterised by fast growth (1off), slow growth (4off), no growth (4off) and fast decay (6off) automata respectively. These proportions were similar to those of niche $1D$ (see Chapter 4) and confirmed that the computation niche model was producing the expected behaviour of a one-state automata population under well-mixed conditions. The reason why niche $1D$ was reproduced rather than niche $1A$ was examined in detail and the findings are presented in Appendix 12.3.

On average the membrane automata were active 64.6% of the time:

The production of population automata for each of these activity groupings were:

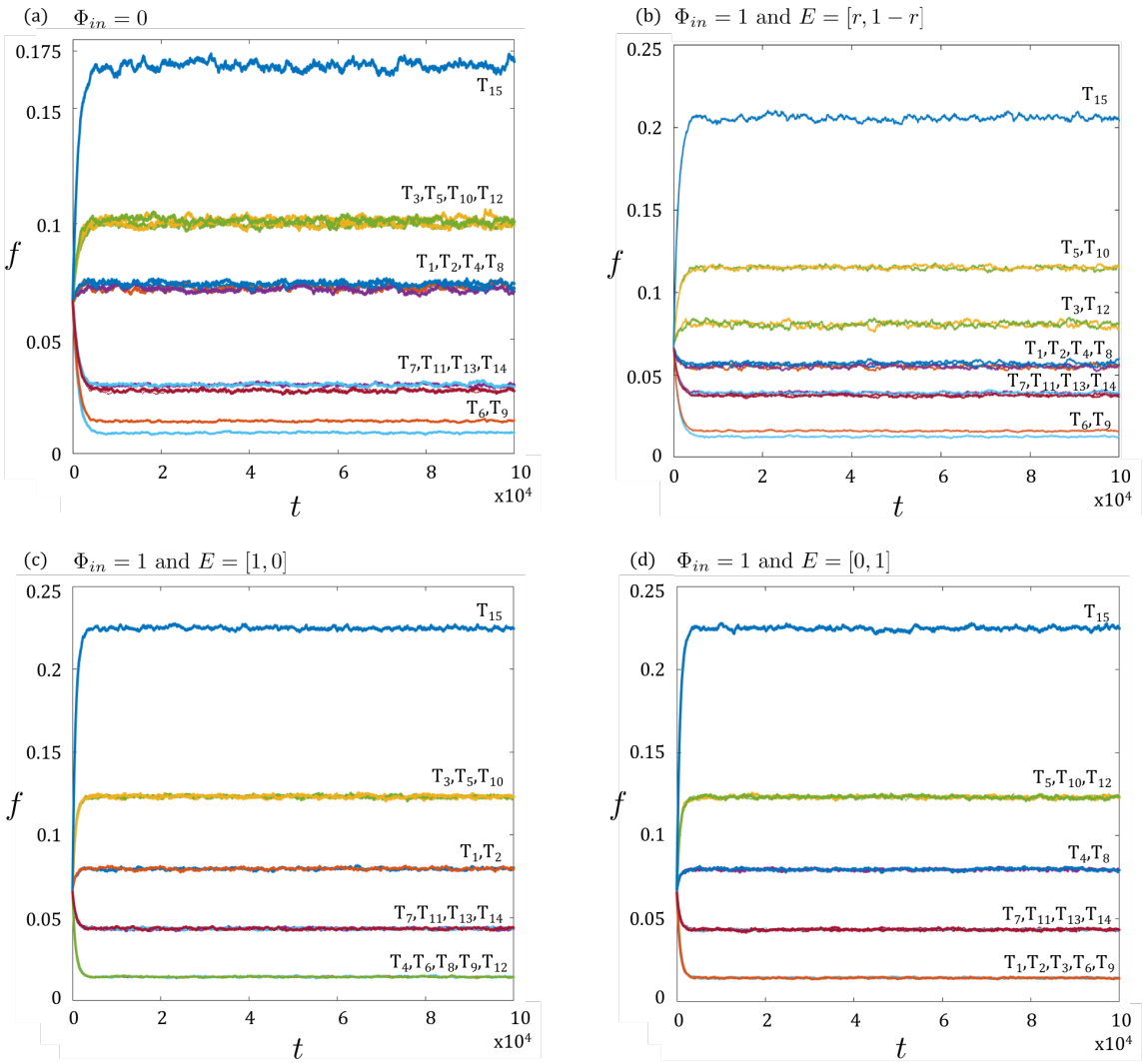


Figure 8.3: The steady-state population structure of the computation niche model after 1×10^5 iterations with and without environmental noise: (a) the steady-state population with no environmental noise ($\Phi = 0$) was very similar to the one-state information niche $1D$ population structure; (b) a constant environmental noise that switched randomly from '0' and '1' led (where the randomly generated number $r \leq 0.5$ indicated the generation of the '0' symbol and $r > 0.5$ generated a '1' symbol) to a significant drop in the concentration of six automata (that were all mono input automata) to generate a new steady-state structure; (c) a constant '0' was emitted as environmental noise and this led to the drop in concentration of all automata that could only process '1' symbols; (d) a constant '1' was emitted as environmental noise and this led to a reduction in those automata that could only process '0' symbols. For (b)-(d) the environmental aperture was set to $\Phi = 1$ hence membrane automata were only processing environmental information.

group	membrane automata	time active
A	M_1,M_2,M_3,M_4,M_8,M_{12}	67%
B	M_5,M_6,M_7,M_9,M_{10},M_{11},M_{13},M_{14},M_{15}	63%

Table 8.3: Examination of the activity within the membrane showed that seven membrane automata were active for 67% of the time and nine were active for 63% of the time.

group	automata produced (f)	total f
A	$T_1(4)$, $T_2(4)$, $T_3(4)$, $T_4(4)$, $T_8(4)$, $T_{12}(4)$	0.49
B	$T_5(13)$, $T_6(2)$,$T_7(6)$, $T_9(2)$, $T_{10}(13)$, $T_{11}(6)$, $T_{13}(6)$, $T_{14}(6)$, $T_{15}(27)$	0.51

Table 8.4: Examination of the activity within the membrane showed that seven membrane automata were active for 67% (Group A) of the simulation and nine were active for 63% of the time (Group B). Simulating these groups separately showed that their activation in the membrane only led to production of themselves in the internal population indicating a strongly connected network components. The number in brackets indicate the number of times that automata type could be produced from the interaction network of which it was a member.

The following observations were made:

- the interaction matrix (G) for these two groups were strongly connected components i.e. each member of the group was produced by other members of the group exclusively. The final frequency distribution (total f in Table 8.4) showed a near even split in the population between the two groups and yet group A consisted of 50% less membrane automata than group B. This suggested a link between the activity of a membrane automaton and the success (or not) of the production of its equivalent population automaton i.e. a more active membrane automaton leads to its equivalent population automaton being more successful in getting replicated

- the membrane matrix (M) revealed that the group A automata had less incoming edges than those in group B ($k_{in} = 12$ compared to $k_{in} = 15$ respectively)

- the weightings on the membrane network showed that the group A edge weightings were lower than the group B network weightings. In general terms the higher the weighting on an edge the more that the information communicated over that edge influenced the activation behaviour of the receiving (target) automata. In this case the effect of the edge weightings were counterintuitive - the lower weighted edges in group A were activating their receiving automata more frequently. This disparity can be explained as follows: the weightings signify the 'amplitude' of the information being sent over that edge, and not the fit between the range of information that can be sent over that edge and the domain of the automata receiving it. Hence,

membrane automata that could alternate between emitting a '0' or a '1' (so-called dual output automata) would sometimes emit information that was of no value to the receiving vertex e.g. automaton T_6 emitted a '0' or a '1' over its outgoing edges to all other automata in the membrane network and for those automata that could only receive one of those symbols there were occasions where no information was received as it could not 'read' all the information emitted by T_6. This negating effect of information on receiving automata was not restricted to mono input automata. Given that dual input channel automata could receive information from all other membrane automata there were occasions where they would receive competing information e.g. a '0' over one edge and a '1' over another edge. Such competition between information sources caused interference that decreased the input probability distribution received by a membrane automaton which subsequently decreased the probability of that automaton surpassing its activation threshold. Dual output automata had this effect on all automata in the network and the difference between the activity of automata in group A compared to group B was simply because they had less incoming connections to other automata in the membrane which translated into less interference (from competing information sources) at their inputs. This suggested that simpler automata were less effected by competing information sources by virtue of their lower information processing properties i.e. they were less susceptible to 'noise' from the other membrane automata.

8.3.2 The effect of constant random environmental noise on production dynamics

A computation niche consisting of 90,000 one-state population automata and 15 one-state membrane automata were simulated for 1×10^5 with $\Phi_{in} = 1$ and $E = [r, 1-r]$ where r was a real number in the range $0 \leq r \leq 1$ randomly generated on each iteration. As such, the environmental input to a membrane automaton was a probability distribution and not an absolute value of '0' or '1'. The time-series of the frequency distribution of the population automata is shown in Figure 8.3b and the change in membrane activity shown in Figure 8.4.

The structure of the steady-state population was similar to that produced by the computation niche under endogenous information flow only. However there was a noticeable reduction in the production of the automata T_1,T_2,T_3,T_4,T_8 and T_{12}. These automata shared the characteristic of being mono input automata i.e. they could only receive one type of symbol (either a '0' or a '1'). Given that the generation of environmental noise was

sampled from a uniform distribution there were times where environmental information was weighted towards the extremes (e.g. $e = 0$ or $e = 1$) which, for mono input receivers, was detrimental as they were very unlikely to activate - if at all. Whilst this was not a phenomenon exclusive to these automata - the membrane automata in group B were receiving the same environmental information - the group B automata could benefit from the full range of environmental information as they were dual input automata.

Table 8.5 shows a comparison of the *ratio of activity* of each membrane automata when the population was isolated from the environment (with $\Phi = 0$) and when it was receiving randomly generated environmental information (with $\Phi = 1$ and $E = [r, 1-r]$).

automata	$\Phi = 0$	$\Phi = 1$	difference
set A	0.33/0.67	0.42/0.58	± 0.09
set B	0.37/0.63	0.34/0.66	± 0.03
	inactive/active	inactive/active	

Table 8.5: Comparison of the average activity of membrane automata (i.e. active or inactive) under isolated ($\Phi = 0$) and random environmental noise ($\Phi = 1$ and $E = [r, 1-r]$) conditions. A significant reduction in the activity of the group A membrane automata in the presence of environmental noise was due to the limited processing of the mono input automata that constituted this group. By comparison, the group B automata were more active in the presence of environmental information.

As can be seen, the presence of environmental information reduced the activity of the automata in set A and increased the activity of the automata in set B. This indicated that the mono input channel automata (group A) were more sensitive to changes in environmental information. The converse was that the dual input channel membrane automata (group B) were less effected by the environment and, indeed, benefited as they were able to process a wider range of inputs and, as such, their activity levels increased. The additional uncertainty introduced by the presence of environmental noise disrupted the normal operation of the membrane to the detriment of the simpler automata from group A and to the benefit of the more complex information processing automata of group B.

8.3.3 The effect of constant environmental noise of fixed value on production dynamics

Two simulations were run of a computation niche consisting of 90,000 one-state population automata and 15 one-state membrane automata for 1×10^5 iterations with $\Phi_{in} = 1$ and $E = [1, 0]$ and $E = [0, 1]$ respectively. Such values for E indicated that the probability of the environment transmitting a '0' symbol or a '1' symbol was certain over the duration of the simulation. The time-series of the frequency distribution of the population automata with

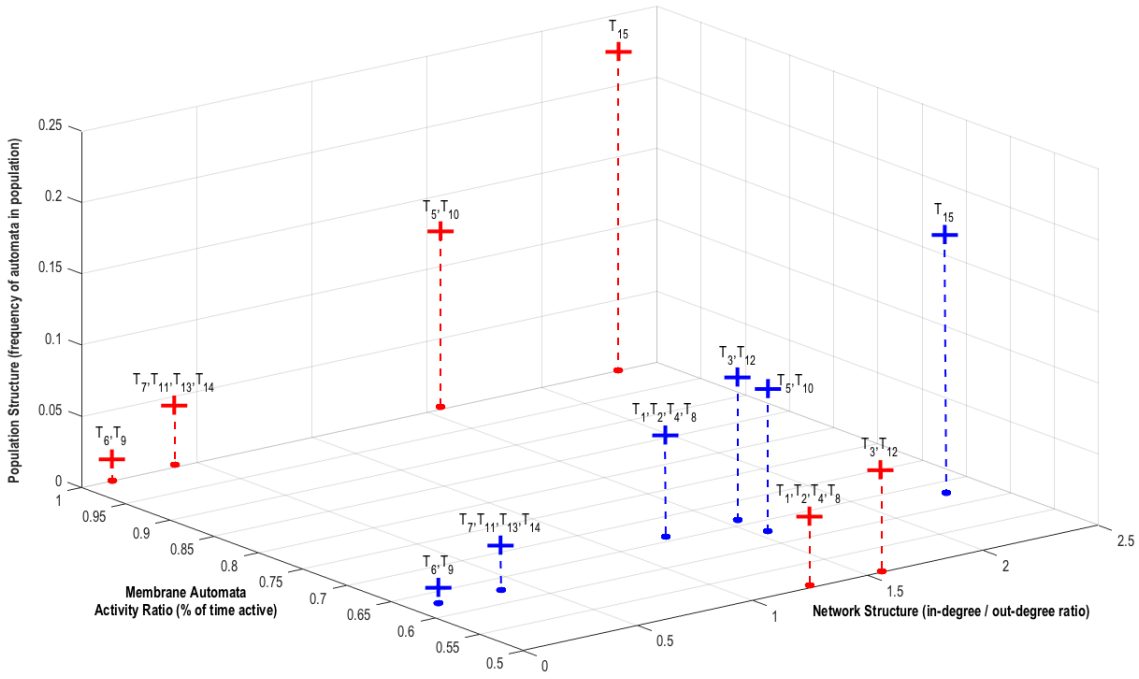


Figure 8.4: Comparison of the behaviour and structure of the internal population with (red) and without (blue) environmental noise effecting the membrane automata. Environmental noise had the most effect on the activity of membrane automata - in the absence of any environmental noise the activity range of membrane automata were tightly grouped in the range 63% to 67% of the time, compared to the range 50% to 100% of automata active over the duration of the simulation with environmental noise. Such a difference in membrane behaviour resulted in a different population structure with the automata $\{T_5, T_6, T_7, T_9, T_{10}, T_{11}, T_{13}, T_{14}, T_{15}\}$ increasing in concentration and the automata $\{T_1, T_2, T_3, T_4, T_8, T_{12}\}$ decreasing in concentration.

environmental noise at the fixed value of '0' is shown in Figure 8.3c and at the fixed value of '1' is shown in Figure 8.3d.

With environmental noise as a constant '0' there was a significant reduction of the automata T_4,T_8 and T_{12} in the population. These automata could only process a '1' symbol and were never activated during the simulation whilst all other automata were constantly active.

With environmental noise as a constant '1' only those membrane automata that could process a '1' symbol were active during the simulation. As such, those automata that could not process '1' (T_1, T_2, T_3) were never activated.

In both simulations the inactive membrane automata were also poorly produced in the internal population. Examination of the interaction matrix showed that under normal conditions (i.e. in the absence of environmental noise) the population automata T_1, T_2, T_3, T_4, T_8 and T_{12} were heavily involved in their own production either as self-replicators (T_1,T_8) or in interactions with each other. However, due to the inactive nature

of their membrane counterparts under constant environmental noise of a fixed value, the number of interactions in the population that could produce them decreased drastically from 60 interactions producing 15 each of T_1,T_2,T_4,T_8 to just 8 interactions producing two of each, and from 42 interactions producing 21 each of T_3 and T_{12} to just 4 interactions producing two of each. The constant environmental noise of a fixed value decimated the production of population automata for those membrane automata that remained inactive due to their mono input channels.

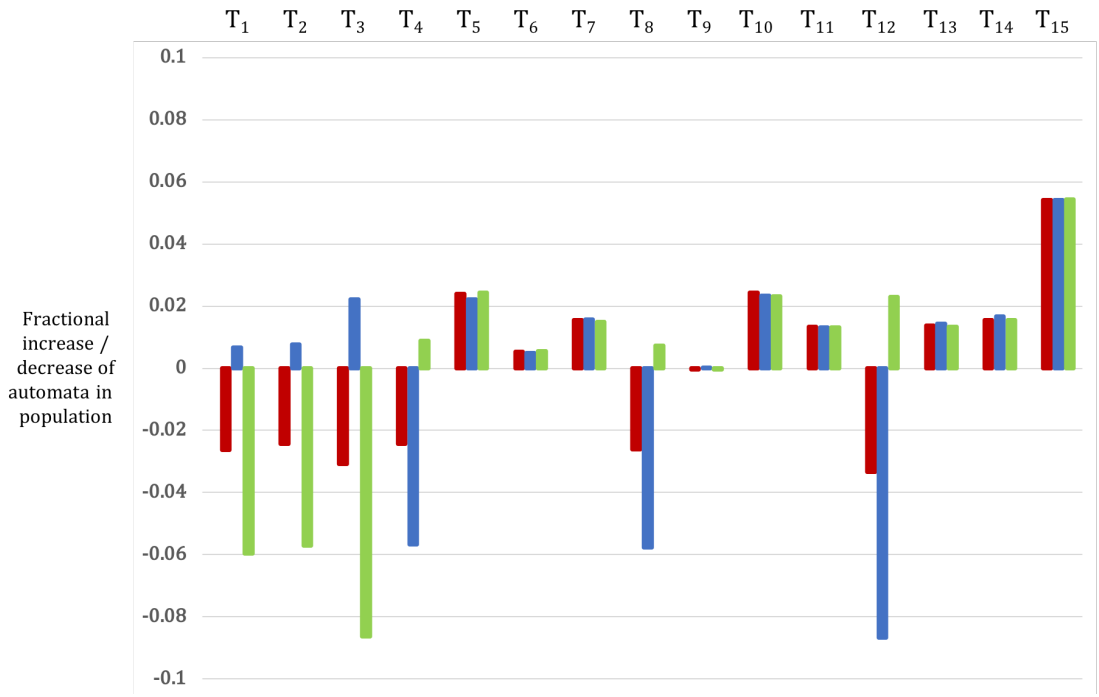


Figure 8.5: Changes in the final frequency of each automata type as a result of changes in environmental noise. The baseline (at zero) was the frequency distribution of the population in the absence of environmental noise. The +/- fractional change in frequency of each automata type is shown in the presence of random environmental noise (red), fixed '0' environmental noise (blue), and fixed '1' environmental noise (green). Those automata with minimal changes across all three environmental noise settings were deemed to be more robust to environmental noise. Group A automata (mono input) are T_1,T_2,T_3,T_4,T_8,T_{12} and the remainder are Group B automata (dual input). As can be seen the frequency of the Group A automata were considerably more sensitive to environmental noise than the Group B automata.

Figure 8.5 shows the fractional change in the frequency of each population automata for each of the three environmental noise conditions examined and illustrates that the automata in the computation niche responded in three different ways to environmental noise: (i) the production of T_6 and T_9 were relatively unperturbed with minimal changes to their level of concentration in the population, (ii) the production of T_5,T_7,T_{10},T_{11},T_{13},T_{14},T_{15} benefited from the presence of environmental noise (as dual input automata) by success-

fully occupying a greater part of the population, and (iii) the production of T_1,T_2,T_3,T_4,T_8 and T_{10} were heavily influenced by the prevailing environmental information that under random or fixed value conditions led to some automata (T_3,T_{12}) losing over 8% of the population to other automata. Those automata in (i) and (ii) were part of group B (dual input automata) and those in (iii) were part of group A (mono input automata) indicating that automata with a wider 'language' were more robust to the presence of environmental noise.

8.3.4 Examining the information processing capacity of automata and sensitivity to environmental noise

There was an association between the information processing capacity (ϱ)[3] of a membrane automata, its sensitivity to environmental noise and the subsequent effect this had on the production of new automata. Consider Table 8.6 which show the one-state automata allocated into one of three partitions based on their ϱ values, and Figure 8.6 which illustrates the flow of production between those partitions.

Partition	$\varrho(T_i)$	automata	% activity change	edges (e)	interactions
1	1 bit	T_1,T_2,T_4,T_8	9% reduction	1	24
2	1.6 bits	T_3,T_5,T_{10},T_{12}	9% reduction	2	27
3	2 bits	T_6,T_9 T_7,T_{11},T_{13},T_{14} T_{15}	3% increase	2 3 4	30

Table 8.6: The one-state automaton types partitioned into three groups dependent on their information processing capacities as measured by their respective ϱ values.

Analysis of the behaviour of objects within and across these partitions revealed that interactions were adhering to the following condition:

Condition: If $\varrho(T_a) > \varrho(T_b)$ then $\varrho(T_c) \leq \varrho(T_a)$

T_a,T_b automata could not create a T_c automaton of greater information processing capacity than the interacting automaton with the highest ϱ. The only exception to this was in the production of T_{15}. It was not always the case that the T_c automaton would inherit the information processing capacity of the T_a,T_b automaton with the highest ϱ.

Conversely, higher ϱ automata could create an automaton with a lower ϱ. This indicated that the production of automata flowed in two directions: downwards e.g. from partition 3

[3]See section 3.5.5 for a reminder of this measure.

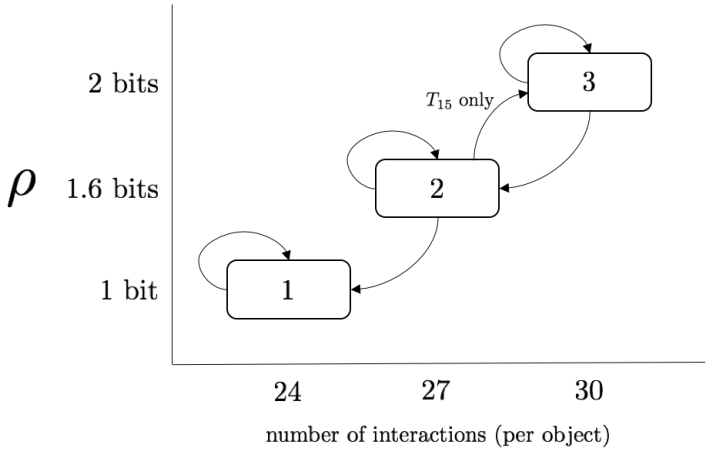


Figure 8.6: Partition map showing the flow of production of new automata between the partitions. In general, production flows either downwards to partitions of lower information processing capacity (ϱ) or horizontally within a partition. In only two cases - $T_5 \circ T_3 = T_{15}$ and $T_{12} \circ T_{10} = T_{15}$ from partition 2 - did production flow upwards to a higher partition due to the multiplicative effect of the functional composition of two automata.

to all other partitions and from partition 2 down to partition 1, and (b) horizontally within a partition.

There was no upward flow of production between partitions with the exception of partition 2 automata to T_{15} in partition 3. This was due to the multiplicative nature of producing a new automaton e.g. the functional composition of two automata with each having only one edge (e) could only create a new automaton with a maximum of $e_{max} = 1 \times 1 = 1$ transitions with one having two edges, $e_{max} = 2 \times 1 = 2$ and $e_{max} = 1 \times 2 = 2$ transitions. However, with each automaton having two edges then $e_{max} = 2 \times 2 = 4$ transitions and this latter case was how T_{15} could be constructed from partition 2 automata (which were all two transition automata).

Furthermore, automata with three transitions could not be created by 1-transition or 2-transition automata. This explained why the automata in partition 3 (with the exception of T_{15} which was a 4-edge automaton) performed so poorly in replication. They were only produced from horizontal production flows within their partition and they also participated in downward production flows which benefited objects in the lower ϱ partitions which was not reciprocated. To summarise, production flow occurred where (a) the complexity of either T_a or T_b was equal to that of the T_c except where (b) the multiplicative effect of functional composition led to the creation of more information processing capacity and this was only possible when both T_a and T_b consisted of at least 2 transitions each.

The information processing capacity (ϱ) measure was only applicable to examination of individual states of an automata as it was a measure of the scope of interactions

that an automata could undertake at that time (i.e. it's interaction potential). As such, its usefulness in analysing multi-state automata was very limited as the information processing capacity was determined by the present state of the automaton. In multi-state automata the information processing capacity of the membrane automata varied dependent on its present state and the alphabet that could be processed whilst in that state i.e. it's information processing capacity was determined by the possible transitions from its present state.

8.3.5 The effect of varying the magnitude and the type of environmental noise on production dynamics

To further understand the relationship between the environment and population structure 11 simulations were run under various environmental conditions. Starting with constant environmental noise of '0' the population was evolved with the environment aperture set to $\Phi = 0.5$ and the frequency distribution of each automaton was noted after 1×10^5 iterations. This was repeated for each increment of E from $(1,0)$ in 0.1 increments to $(0,1)$. The results are shown in figure 8.7.

The reference point at $P(E) = (0.5, 0.5)$ in Figure 8.7 - which is the midpoint of the x-axis - was where the population's frequency distribution most closely aligned to the structure of the computation niche in the absence of environmental noise. Production of some automata were sensitive to changes in the environment e.g. T_3 benefitted from an environment where $P(E) \rightarrow (0,1)$ but fared less well where $P(E) \rightarrow (1,0)$. This was a direct result of environmental information amplifying or inhibiting the information that was received by each membrane automaton. Depending on the processing that occurred at each membrane automata the same environmental information could amplify the activation of an automaton whilst simultaneously inhibiting the activation of another. For example, with $P(E) = (1,0)$ (i.e. $e = 0$) the membrane automaton T_1 - which only accepted a '0' symbol - was more likely to activate than T_2 - which could only accept '1' symbols. This was because of the summation of inputs to each automaton surpassing (or not) the activation threshold. As such, environmental information could reduce the activation threshold for a membrane automaton meaning that it was triggered more frequently, or it could increase the activation threshold thus reducing the chances of that automaton being activated.

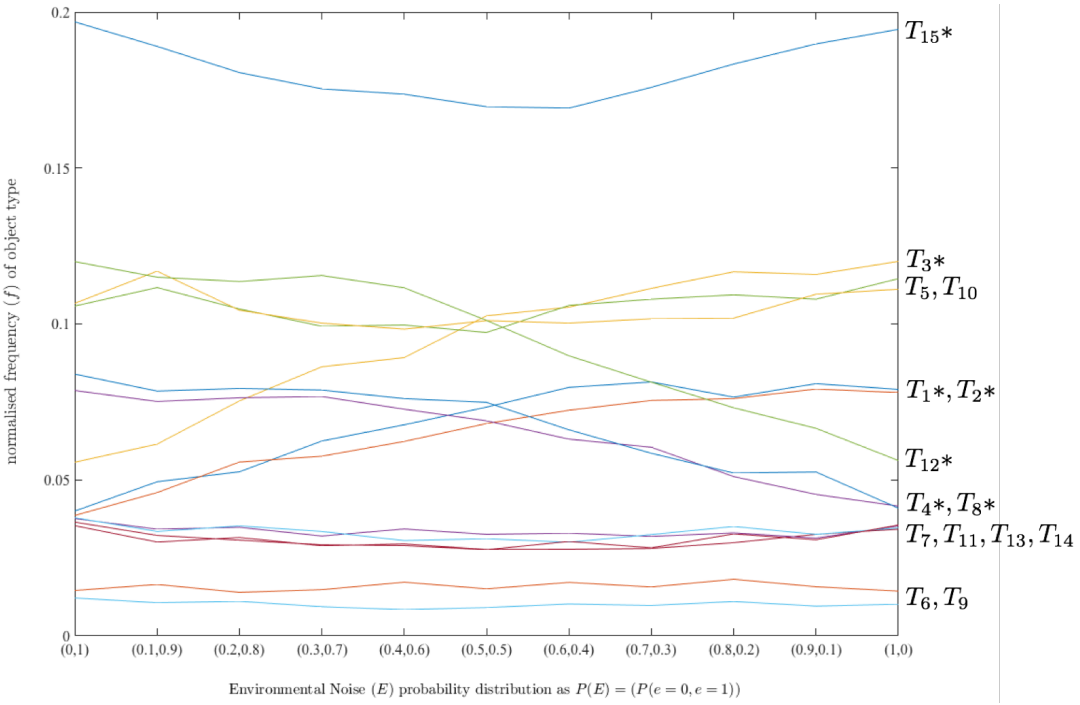


Figure 8.7: The final frequency distribution of automaton types for eleven different environmental settings incrementing from $P(E) = (0,1) \rightarrow P(E) = (1,0)$ and with the environmental aperture set at $\Phi = 0.5$. The production of seven automata (indicated by $*$) were more sensitive to changes in environmental information. The x-axis indicated the environmental information setting used for that simulation run and the y-axis indicated the final frequency distribution of the population automata after 10^5 iterations. The environmental setting of $P(E) = (0.5, 0.5)$ was the closest match to the computation niche that formed in the absence of environmental noise.

8.3.6 Examining the intensity of environmental noise on production dynamics

To examine the effect of the intensity of the flow of information from the environment on automata production - the influx rate Φ_{in} - the previous simulation (of examining the final frequency distribution of the population for different types of information from the environment) was repeated for various values of Φ_{in} where $0 \leq \Phi_{in} \leq 1$ in increments of 0.1. This required 121 simulations: 11 simulations for E from $E = [1,0] \rightarrow E = [0,1]$ in 0.1 increments for each of 11 different values of Φ_{in}. Each simulation was run for 1×10^5 iterations. The results are shown in Figure 8.8.

As to be expected when $\Phi_{in} = 0$ (no environmental noise and where the niche was exclusively processing endogenous information) there was little difference between successive values of E because environmental information had no effect on population dynamics and the variation in frequency of population automata was due to the stochastic nature of the

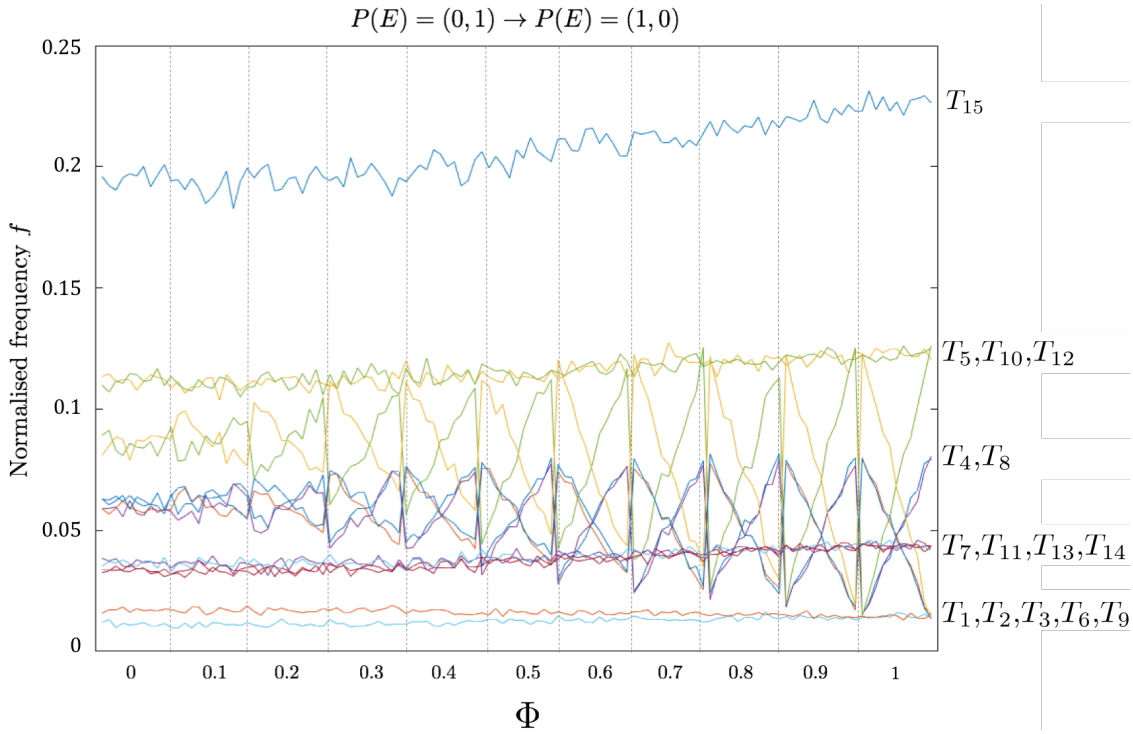


Figure 8.8: The level of structural change that was occurring within the niche was dependent on the rate of information flow into the niche from the environment. The y-axis shows the frequency of occurrence of an automata type at the end of the simulation. Each column - separated by a vertical dotted line - showed the results from 11 simulations for various environmental values for a given value of Φ_{in} as indicated on the x axis. For example, for each of the 11 simulations for a given Φ_{in} the environmental information was incremented from $P(E) = [0,1] \rightarrow P(E) = [0,1]$ in 0.1 increments. For each simulation the computation niche was allowed to evolve for 10^5 iterations at which point the frequency of each automata type was recorded. There were three types of observed changes in the structure of the niche. Group B automaton types were produced more frequently as $\Phi_{in} \rightarrow 1$, whilst Group A automaton types experienced drastic oscillations in their rate of production as a result of environmental information and an increasing value of Φ_{in}. The rate of production of the two automaton types (T_6, T_9) converged at $\Phi_{in} = 1$.

membrane activation process. With $0 < \Phi_{in} \leq 1$ the scale of the variation that occurred in production increased as $\Phi_{in} \rightarrow 1$ for those membrane automata that were more sensitive to environmental information e.g. the group A automata.

8.3.7 The effect of modulating environmental noise with emissions from the niche

To examine the effect of emissions from the niche ($\mathcal{N}$) entering into and modulating the environment five successive simulations were run with the following out-flux rates $\Phi_{out} = \{0, 0.25, 0.5, 0.75, 1\}$ respectively and with the rate of environmental noise into the niche set to $\Phi_{in} = 1$ throughout. The time-series data of the environmental information was

captured on each iteration of the simulation and this was used to generate a histogram with the value of each data point allocated into 1 of a 100 bins. This resulted in a distribution of the likely environmental information values received by the membrane over the duration of the simulation. The histogram values were normalised and the Shannon entropy of the resultant normalised frequency distribution was calculated:

Φ_{out}	$H(E)$(bits)
0	6.64
0.25	6.48
0.5	6.26
0.75	5.94
1	6.21

Table 8.7: The Shannon entropy of the environment $H(E)$ for increasing rate of emissions from the computation niche (Φ_{out}).

In general as the rate of niche emissions into the environment increased (as indicated by a higher value for Φ_{out} in Table 8.7) the greater the reduction in the entropy of the environment. However, there was an increase in environment entropy with $\Phi_{out} = 1$ as the environment was now fully mirroring the structure of the niche which had a flatter distribution than the one seen in the environment with $\Phi_{out} = 0.75$. Several subsequent re-runs of the simulation in the range $0.75 \leq \Phi_{out} \leq 1$ identified that there was a steady increase in environment entropy as $\Phi_{out} \rightarrow 1$. Hence, emissions from the niche at the rate $\Phi_{out} = 0.75$ was the most effective at reducing the entropy of an environment that was randomly generating binary information (see Figure 8.9).

The emissions from the niche were decreasing the Shannon entropy of the environment thus reducing uncertainty about its next most likely transmission. Hence, the niche was ordering the environment which - given the bi-directional flow of information between the niche and the environment - meant that the behaviour of the membrane should also become more predictable. There was a noticeable effect on the population dynamics when environmental information was being modulated by emissions from the niche (see Figure 8.10) that were similar to that observed when simulating the effect of random environmental noise on membrane activity (see Figure 8.3b). Although there were slight changes in the structure of the population for various values of $\Phi_{in,out}$, the Shannon entropy of the frequency distribution of automata at t_{max} was ≈ 3.6 bits in all cases indicating that the identity of the computation niche was retained under the influence of environmental noise that was being modulated by emissions from the niche itself via. the membrane.

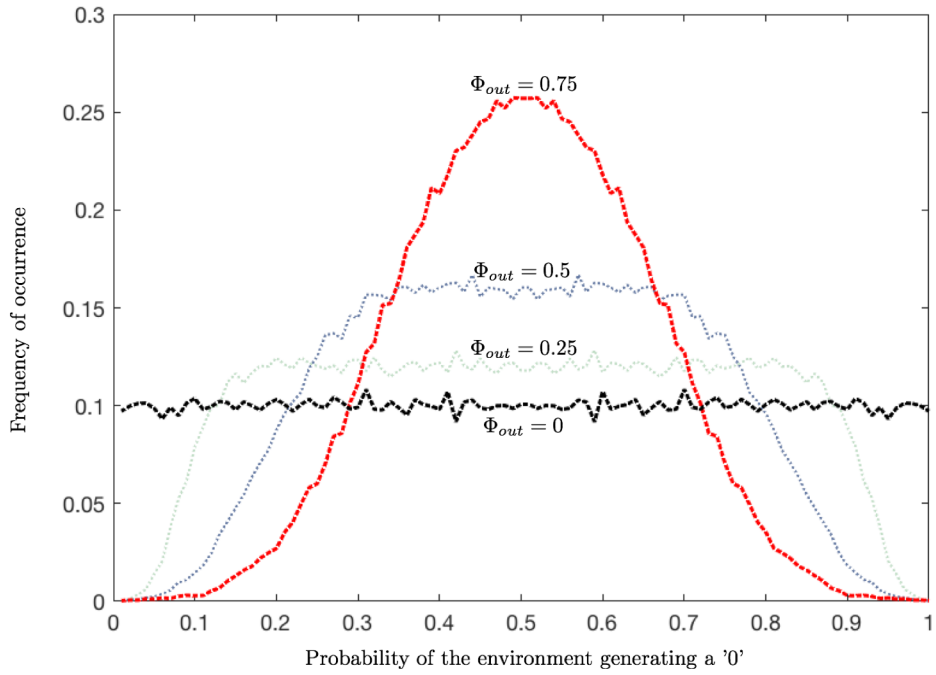


Figure 8.9: Histogram of the value of E throughout four different simulations with varying values of Φ_{out}. The stronger the coupling of the niche to the environment the greater the reduction in the Shannon entropy generated in the environment up to a maximum of $\Phi_{out} = 0.75$. Higher rates of niche emissions ($\Phi_{out} > 0.75$) into the environment led to a subsequent increase in entropy due to the environment increasingly mirroring the niche emissions.

To examine the effect of various values for $\Phi_{in,out}$ on the entropy of the niche emissions and environmental noise, 121 simulations were run for 1×10^5 for values of $\Phi_{in} = \{0.1, 0.15, ..., 0.95, 1\}$ and $\Phi_{out} = \{0.1, 0.15, ..., 0.95, 1\}$. The history of the niche emissions and environmental noise during these simulations were used to estimate their respective entropy ($H(E)$ and $H(\mathcal{N})$). The results were mapped according to the value of Φ_{in}, Φ_{out} and H as can be seen in Figure 8.11a for the entropy of the environment and Figure 8.11b for the entropy of the niche emissions.

The environment entropy map showed a steep reduction in entropy as $\Phi_{out} \rightarrow 0.75$ before increasing in entropy from $0.75 < \Phi_{out} \leq 1$. This was consistent with the earlier finding that demonstrated niche emissions reduced the entropy of the environment. There was one instance, with $\Phi_{in} = 1, \Phi_{out} = 0.75$, where there was a sudden reduction in entropy from 5.8 bits down to 5.6 bits.

The niche entropy map showed a shallower profile with entropy decreasing with $\Phi_{in} \rightarrow 0$ which suggested that the intensity of environmental noise on the membrane (Φ_{in})

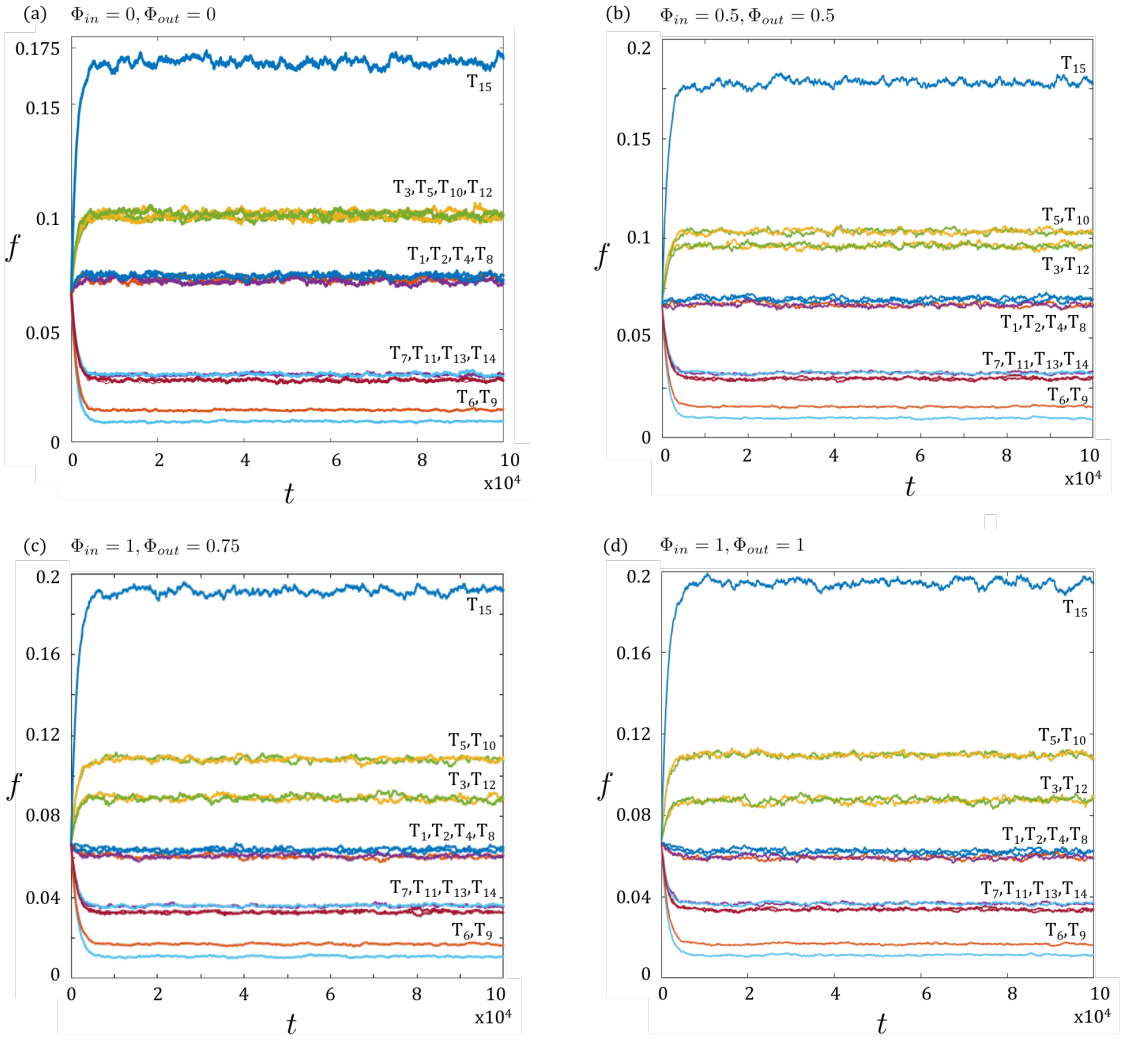


Figure 8.10: The time-series plots of the frequency distribution of the computation niche population over 1×10^5 iterations for various $\Phi_{in,out}$ values: (a) the nominal population structure of the computation niche under endogenous information flow conditions with $\Phi_{in} = 0, \Phi_{out} = 0$; (b) the population structure where a partial exchange of information between the environment and the niche was occurring with $\Phi_{in} = 0.5, \Phi_{out} = 0.5$ leading to some separation of the T_3, T_5, T_{10}, T_{12} concentrations with the reduction in number of the T_3, T_{12} automata due to their only processing single symbols (e.g. '0' or '1' but not both); (c) the population structure where information flow within the computation niche membrane was solely from environmental noise ($\Phi_{in} = 1$) and with the environmental noise itself mostly influenced by the emissions from the niche ($\Phi_{out} = 0.75$). As can be seen there was a greater reduction in the production of T_3, T_{12} compared to (b); (d) the population structure where the 'information coupling' between the niche and the environment was total i.e. the membrane of the niche solely processed environmental noise ($\Phi_{in} = 1$) and emissions from the niche completely determined environmental noise ($\Phi_{out} = 1$) thus creating a closed cycle of information flow. As can be seen there was a reduction in the production of T_3 and T_{12}.

increased the uncertainty of the behaviour of the computation niche (as reflected in a higher entropy of its emissions). Similarly, there was a sudden drop in entropy at the exact same point as was observed in the environment entropy niche map ($\Phi_{in} = 1, \Phi_{out} = 0.75$).

Figure 8.12 reproduced the simulation data where $\Phi_{in} = 1$ and various values of Φ_{out} in the range $0.05 \leq \Phi_{out} \leq 1$ were increased in 0.05 intervals. Four states of the computation niche and environment were identified:

(i) with $H_E > H_{\mathcal{N}}$ the environmental entropy decreased at a faster rate than the niche entropy was increased

(ii) there was a crossover point at $\Phi_{out} = 0.45$ where $H_{\mathcal{N}} > H_E$ at which the environment and niche entropies continued to decrease and increase respectively

(iii) with $\Phi_{out} = 0.75$ there was a sudden decrease in both entropies to the extent that the entropy of the emissions from the niche were now lower than that of the environment

(iv) from $\Phi_{out} = 0.8 \rightarrow 1$ the entropy of both returned to a value close to that prior to (iii), however, the environmental entropy began to increase and at $\Phi_{out} = 1$ the entropy of both the niche and the environment were identical

Whilst the environment entropy changed significantly for all values of Φ_{out} the niche entropy remained relatively stable throughout (with the noted exception at $\Phi_{out} = 0.75$). The niche entropy with $\Phi_{out} = 0.05$ was 6.08 bits and with $\Phi_{out} = 1$ was 6.15 bits compared to the environment entropy of 6.6 bits and 6.15 bits respectively. The matching entropies $H_{\mathcal{N}} = H_E$ with $\Phi_{in} = 1, \Phi_{out} = 1$ were anticipated as the membrane automata only received information from the environment and the environment exactly matched the emissions from the niche. The highest ratio of $H_{\mathcal{N}}/H_E$ was 1.03 with $\Phi = 0.65$ and the lowest was $H_{\mathcal{N}}/H_E = 0.92$ with $\Phi = 0.05$. According to Fernandez et al. [140] when $H_{\mathcal{N}}/H_E > 1$ then the system (as represented by its emissions $\mathcal{N}$) is acting autonomously within its environment (E) and they suggest that this indicated an autopoietic system.

The sudden change in the environment entropy and niche entropy at $\Phi_{out} = 0.75$ warranted further study. As such, additional work was carried out to examine the change in the entropy of environmental noise and the entropy of niche emissions within the narrow range $0.7 \leq \Phi_{out} \leq 0.8$. By increasing the value for Φ_{out} in small increments of 0.002 across this range, an additional 50 simulations of the computation niche were run. The results for measuring the entropy of environmental noise are shown in Figure 8.13. As can be seen the change in entropy is sudden and not gradual. Measuring the entropy of the niche

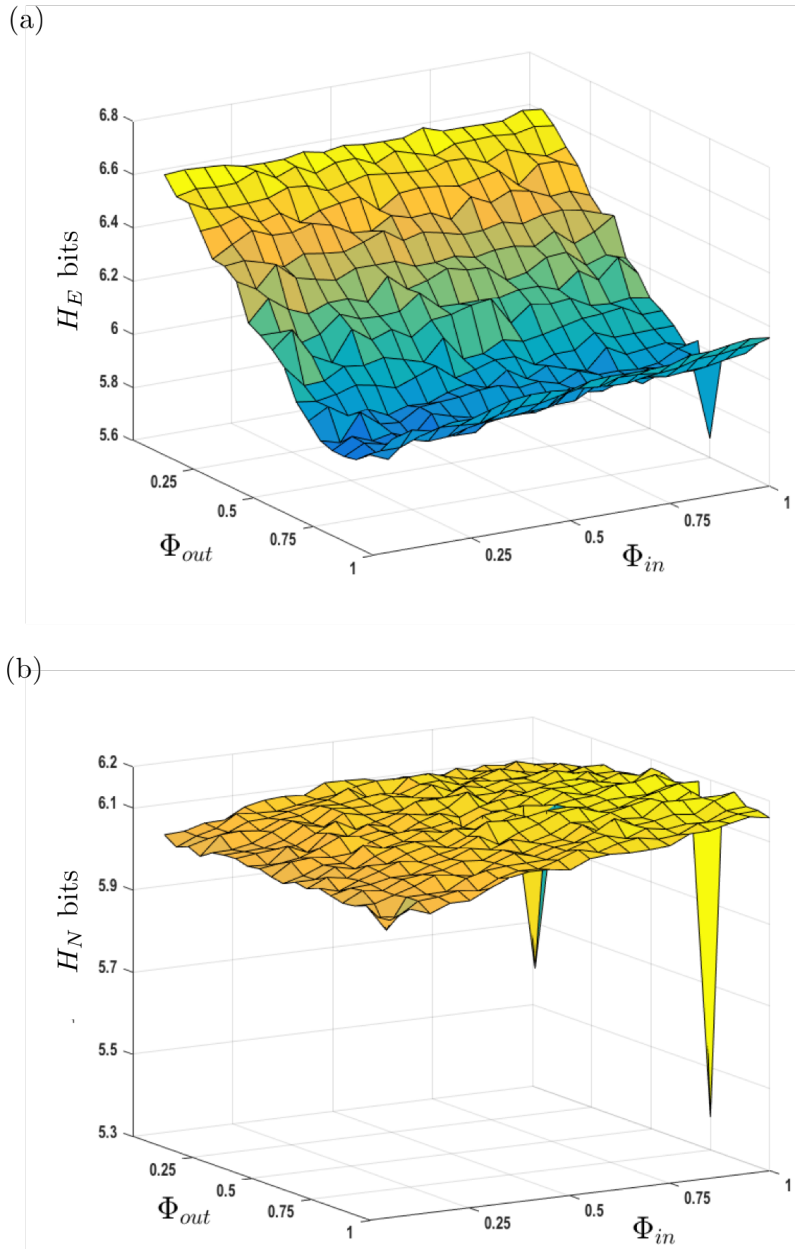


Figure 8.11: Maps of the environment and niche entropy measurements over 121 simulations for various values of Φ_{in}, Φ_{out}: (a) the environmental entropy map showed a consistent decrease in entropy across all values of $0 \leq \Phi_{in} \leq 1$ and with $0 \leq \Phi_{out} \leq 0.75$. However, there was a steady increase in environment entropy in the range $0.75 < \Phi_{out} \leq 1$. The mean environment entropy was $< H_E >= 6.18$ bits with a maximum of $H_E^{max} = 6.6$ bits and a minimum of $H_E^{min} = 5.67$ bits; (b) the niche entropy map showed a shallower profile where the entropy steadily increased as $\Phi_{in} \rightarrow 1$. There was a significant dip in entropy to its lowest point at $\Phi_{in} = 1, \Phi_{out} = 0.75$ which corresponded exactly with the minimum entropy point of environmental entropy. The mean niche entropy was $< H_{\mathcal{N}} >= 6.1$ bits with a maximum of $H_{\mathcal{N}}^{max} = 6.2$ bits and a minimum of $H_{\mathcal{N}}^{min} = 5.38$ bits.

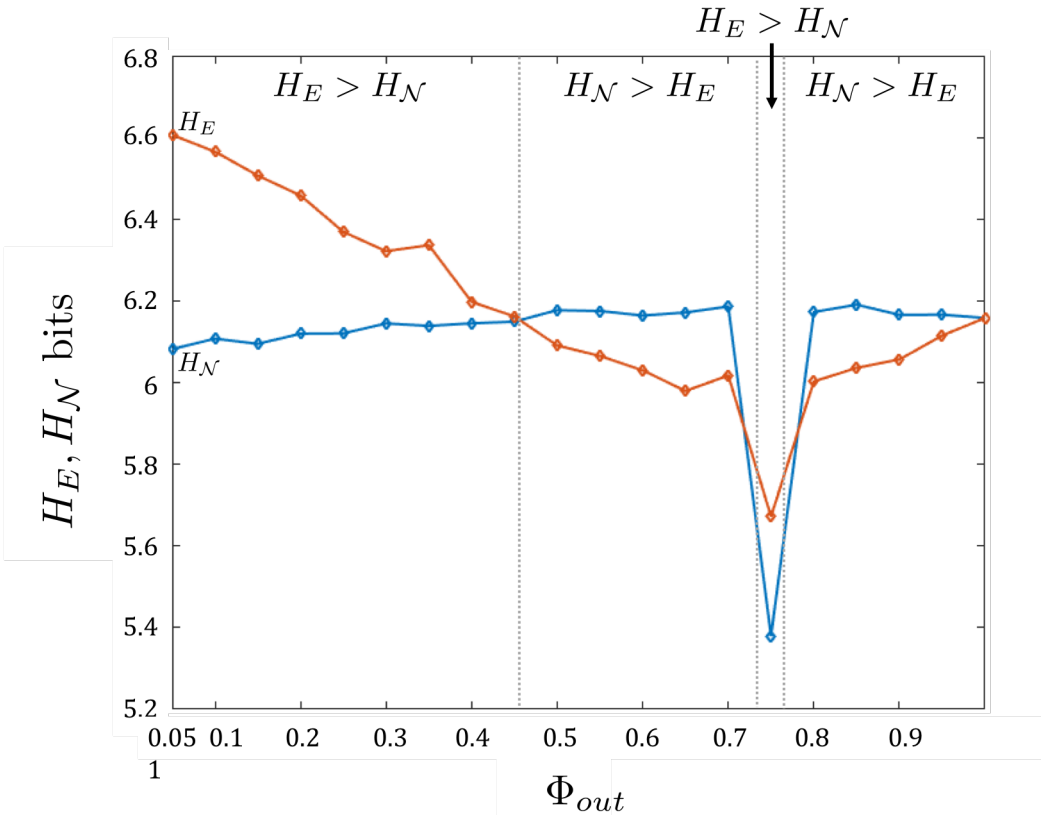


Figure 8.12: A graph comparing the changes in the Shannon entropy of emissions from the niche and the environment over 21 simulations for increasing values for Φ_{out}. At $\Phi \approx 0.75$ there was a distinct drop in the Shannon entropy of both niche and environment.

emissions showed a similar sudden drop in value at $\Phi = 0.75$. This suggested the presence of a phase transition in the computation niche or an anomaly in the model. However, it was clear from Figure 8.13 that there was no indication of any gradual lead in to the reduction in entropy of the niche nor the environment. This could have been the result of a possible error condition being reached in the model. Therefore this result, whilst interesting, could not be deemed to be reliable. A more detailed investigation into the nature of this sudden change in entropy of both the environmental noise and the niche emissions is recommended for future work.

In summary, with emissions of information from the niche at a rate $\Phi = 0.75$ there was a simultaneous reduction in the entropy of both the niche and the environment. This may suggest that the coupling of niche and environment had the effect of increasing the order of both. Further work is required to investigate what effect, if any, this increased structuring of information had on the structure and behaviour of the niche.

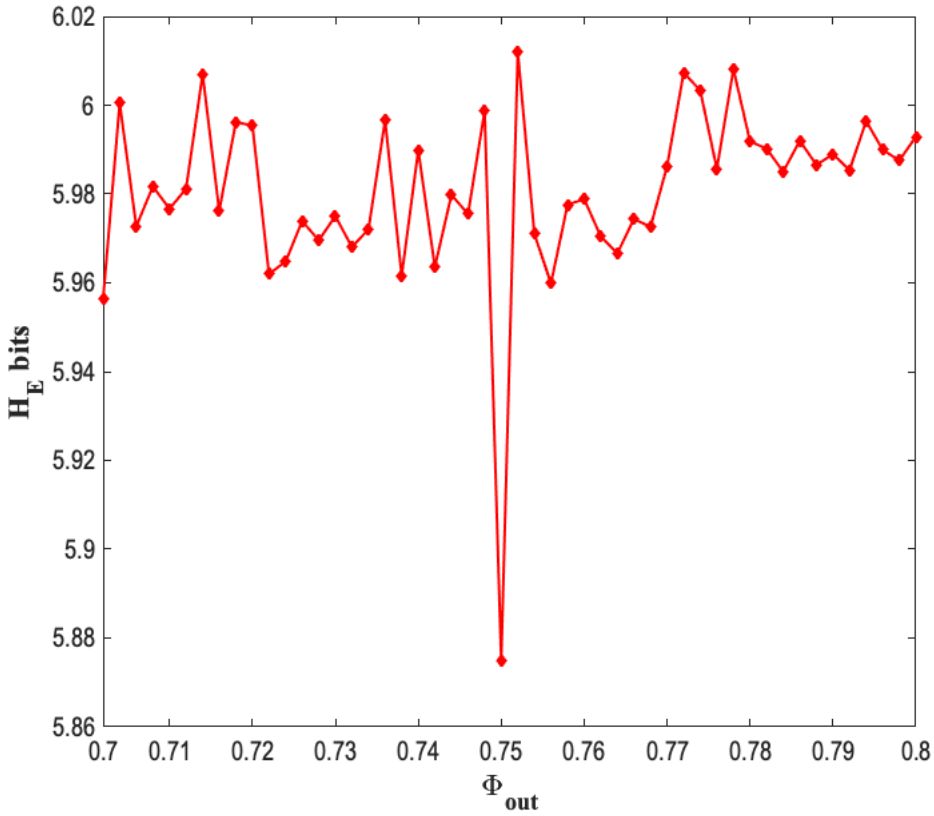


Figure 8.13: The results of an additional 50 simulations of the computation niche detailing the changes in the entropy of environmental noise ($H(E)$) across a narrow range of niche emissions ($0.7 \leq \Phi_{out} \leq 0.8$) with values of Φ_{out} increased in increments of 0.002.

8.4 Analysis of the activity of the membrane

Analysis of the activation history of the membrane's automata showed that a set of membrane states representing the inactive/active status of each membrane automata existed. A state here was the unique configuration of the membrane's automata activation status (i.e. inactive or active) recorded in the 15-element vector Ψ. An algorithm was developed (see Chapter 3) to examine the time-series data of the membrane automata activation status $\overleftarrow{\Psi}$ which had been recorded on each iteration of the simulation. The algorithm identified each unique state that the membrane entered and how often it entered that state during the simulation. This algorithm was executed on the results from four simulations and the results are shown in Table 8.8.

For a simulation of the computation niche in the absence of environmental noise

Φ_{in}	E	No. of Unique States (Σ)	Most Visited	Shannon entropy ($H(\Sigma)$ bits)
0	$\emptyset$	23,811	0.7% (683)	13.7
1	$[r, 1-r]$	22,386	6.3% (6,373)	11.9
1	[1, 0]	1	100%	0
1	[0, 1]	1	100 %	0

Table 8.8: The different states that the membrane could occupy for various environmental settings. The number in brackets indicates the absolute count of the number of times the membrane re-visited the most often visited state.

($\Phi_{in} = 0$) there were 23,811 unique states that the membrane occupied and in the presence of random environmental noise ($\Phi = 1$ and $E = r$) there were 22,386 unique states identified. These were very small when compared to the theoretical maximum number of states which was 2^{15} and very large when compared to the number of states that the membrane occupied in the presence of fixed environmental noise (i.e. $e = 0$ or $e = 1$). It was interesting to note that the presence of environmental noise increased the number of states that the membrane entered during the simulation and also the number of times that the membrane re-visited those states e.g. the membrane network spent 6.3% of its time re-visiting the same network state under random environmental noise compared to the membrane network spending just 0.7% of its time re-visiting a prior state when there was no environmental noise. The Shannon entropy of the distribution of states ($H(\Sigma)$) indicated that the presence of environmental noise was introducing more order into the activity of the membrane ($H(\Sigma_{E=r}) = 11.9$ bits) compared to the membrane acting completely under endogenous conditions ($H(\Sigma_{E=\emptyset}) = 13.7$ bits). This was an interesting result as it suggested that the presence of random environmental noise increased the range and diversity of the activity of the membrane and yet simultaneously introduced a more structured and predictable pattern of behaviour from the membrane than compared to the membrane acting purely under an endogenous information flow (i.e. with no environmental noise). In the context of the membrane as a system interface between a self-producing system and an environment this increased diversity and structured behaviour of the membrane could be important to the system adapting (through assimilation and accommodation) to changes in its environment. This is worth exploring in future work.

By comparison in the presence of constant and fixed environmental noise ($\Phi = 1$ and $E = [1,0]$ i.e. a constant '0' symbol) the membrane occupied and stayed in the same state throughout the simulation. In this recurring state all membrane automata that could process a '0' symbol were activated and all membrane automata that could not process this symbol were de-activated (the three membrane automata M_4,M_8,M_{12}) throughout the simulation. Likewise, with $\Phi = 1$ and $E = [0,1]$ i.e. a constant '1' symbol, the membrane

occupied and stayed in the same recurring state but this time with all '1' symbol processing membrane automata activated and all membrane automata that could not process '1' deactivated (the membrane automata M_1,M_2,M_3) throughout. This represented a complete lack of diversity in membrane activity which was reflected in a Shannon entropy of 0 bits.

On very rare occasions a simulation run of the computation niche in the absence of environmental noise would result in the membrane becoming completely deactivated. This subsequently led to the cessation of any production of new automata within the internal population and, hence, the system effectively 'died'. Examination of the status of the membrane automata immediately prior to this death state did not reveal any kind of unusual activity. One possible explanation is the extremely unlikely scenario whereby none of the membrane automata surpassed their activation threshold simply because the randomly generated number (r) happened to be of a sufficiently high value for all fifteen membrane automata within the same time step. This was a possible state, albeit rare, that the membrane could enter. Over several hundred simulations of the computation niche the 'death state' was observed on four occasions. This was an interesting phenomenon and may indicate that the presence of environmental noise was necessary to reduce or prevent the occurrence of a 'death state' in the membrane. This is discussed further in Chapter 10.

8.5 Cognition and the Computation Niche model

The computation niche model demonstrated a cyclical and hierarchical process where a primitive form of learning occurred with the coupling between the environment, the membrane automata and the population automata reducing uncertainty about the future behaviour of the system based on its previous behaviour and that of the environment. This learning was stored as information in the weightings of the membrane network edges and simultaneously in the frequency distribution of the internal population. If such information represented an internal model of the system and its environment - as suggested by Robert Rosen [72],[89] and his concept of anticipatory systems - then the computation niche was anticipating the next state of itself based on past and present information. Such a system required a continual renewal of the information storage and retrieval processes to maintain a steady-state distribution of information within the system. It appeared that the computation niche model was able to simulate such a dynamical process. Recent developments in information theory such as transfer entropy [141] can be applied to the computation niche model by treating components of the model as connected stochastic processes representing a source and destination information source. From this the transfer entropy method could be used to quantify the information flow between them. Indeed,

analysing and quantifying a complex system as a computation process has been proposed by Lizier et al. [142] and the application of such techniques to the computation niche model is recommended as future research work (see Chapter 10).

The exchange of information between the membrane and the environment demonstrated a basic form of structural coupling [7]. The niche was effecting the environment in a way that contributed to its own operation. This suggested that the operational limits of the computation niche model extended beyond the processes that were defined by the membrane and internal population alone. As such, the computation niche model could be useful for examining "extended autopoiesis" [16]. This concept purports that the operational limits of an autopoietic system should include those external processes that, whilst not created by the system, it is dependent on.

8.6 Summary

This chapter has investigated the effect of a membrane as the interface between an interacting population of self-producing automata and an external environment. The main findings were:

- the membrane had a direct effect on the structure of the population by inhibiting parts of the interaction network of the internal population
- the relationship between the membrane and the internal population was cyclical with activation of membrane automata effecting the production of new automata in the interior which changed the weightings of the membrane network and which subsequently effected the information that was processed by the membrane
- environmental noise interfered with the normal operation of the membrane that, dependent on the processing behaviour of each automata, could inhibit or excite activation of membrane automata
- mono input membrane automata were more sensitive to environmental noise which led to their reduced activation in the presence of random environmental noise and their complete de-activation in the presence of constant environmental noise
- the greater the inhibition of the membrane the greater the change that occurred in the structure of the internal population
- emissions from the niche into the environment modulated environmental noise and this reduced the Shannon entropy of the environment

- fixed probability environmental noise had a noticeable effect on the membrane automata information processing and this led to a change in the population structure. With environmental noise constantly producing a '0' or a '1' this created the largest disturbances to the niche. Conversely, environmental noise that flipped with equal probability between '0' and '1' had a more subtle effect on the population structure. In all cases the degree of disturbance was more pronounced as the magnitude of the noise that was transmitted into the membrane increased (i.e. as $\Phi \rightarrow 1$)

- a niche could 'die' when all membrane automata were de-activated which was extremely rare. In such instances the presence of environmental noise was required to resurrect the membrane automata and prevent any further occurrences. This observation revealed the critical importance that the environment had in perturbing a membrane to prevent it entering a 'death state'

- the computation niche model could be used to model related concepts of autopoiesis such as extended autopoiesis [16], Rosen's anticipatory systems [89] and in understanding how computation occurs in distributed information processing systems [142]

CHAPTER 9

RESULTS VI - NOVELTY IN A MULTI-STATE COMPUTATION NICHE

9.1 Introduction

Chapters 4-8 have investigated the emergence of information and computation niches in populations of one-state and two-state interacting automata. Whilst the results of those simulations were non-trivial, the construction of novel automaton types through endogenous growth was not examined. Interactions between one-state automata could only ever produce other one-state automata, and - given the constraint that all automata must belong to the special class of finite state transducers called ϵ-machines (T) - this constrained the diversity of the population to 15 one-state automaton types (see Chapter 3). By contrast, automata with two or more states (i.e. $\mid Q \mid \geq 2$ where Q was the set of states of an automaton) could interact to generate a new automata that had up to $Q' = \mid Q \mid \times \mid Q \mid$ states. That new automata could then interact with other multi-state automata to create another new automata with $Q'' = \mid Q' \mid \times \mid Q' \mid$ states. And so on. Each new (novel) automata produced by multi-state automata interactions introduced a new information processing function into the population. However, for the reasons discussed in Chapter 5, the simulations of two-state automata were restricted to producing two-state automata only. This chapter describes the results of extending and simulating the computation niche model, to allow unconstrained interactions between multi-state automata. This allowed for the open-ended diversification of the population as new automaton types were produced. Any effect that

increasing the average structural complexity ($< C_\mu(T) >$) and the interaction network complexity ($C_\mu(G)$) of the population had on production dynamics was also examined.

The questions that were being addressed with the open-ended novelty simulations were:

How does novelty arise in an automata population? The ability for interacting automata of the ϵ-machine class with $\mid Q \mid > 1$ states to generate novel automata has been previously reported [134]. What are the population dynamics of an unconstrained multi-state automata population?

What was the effect of novelty? In a population that initially consisted of automata that could self-replicate and where some mutual production was occurring, how did novelty affect an established or emerging population?

How does novelty compare to self-replication as a competitive strategy? Due to the requirement of the computation niche model for a constant population size to be maintained the generation of new automata would displace incumbent automata (some of which were self-replicators and some of which may be new types of automata). Simultaneously, self-replicators were reproducing themselves which also displaced other incumbent automata. Given the synchronous update nature of the computation niche model all possible productions were carried out within a single time step. Changes in the frequency of self-replicating automata and novel automata were recorded during the simulation.

What can novelty tell us about the evolution of self-producing populations? As has been seen with the information niche and computation niche models, with a one-state population there were a finite number of steady-state organisations that persisted (i.e. a niche). These niches could not evolve in the Darwinian sense of the word and, as such, they have been described as pre-evolutionary models. To evolve would require the ability for the population to generate types of automata that were different to themselves and to do so in an unrestricted manner i.e. without any constraints on the type of automata that could be produced. An environment with limited space and limited resources created a competitive pressure that acted as a form of constraint on the type of automata that could persist. The interplay between creating new automaton types and their ability to subsequently persist would provide some insight to how a self-producing system may adapt (through assimilation and accommodation) over time.

9.2 Simulation Setup

The simulation of open-ended generation of novel automata used the computation niche model described in Chapter 8. The ability to generate multi-state automata with no constraints was added to the model. For the reasons explained in Chapter 8 the synchronous update of the population was more appropriate for examining the rate of novelty generation in the population where all possible interactions - and subsequent production of automata - were considered in each time step. By comparison, the asynchronous update of a population only produced one new automaton on each iteration of the simulation and this would omit a significant number of other possible interactions. Hence, in the open-ended simulations reported here at the end of each iteration of the simulation all possible interactions were performed and all valid productions of novel or existing automaton types were accounted for. This represented the maximum development, or progression, of the population as a whole given its current structure and the completion of one full update of the population on each iteration of the simulation was referred to as a *generation* of the population.

The environmental condition experienced by the population was that of a well-mixed environment ($c = N, v = n, \Phi = 0$). Given the primary interest here of examining the generation of novelty within a population, factors such as environmental perturbations or noise were not considered. The population size was fixed at 99,950 automata and initially consisted of 129 one-state and two-state automata that were self-replicators with an ability to produce novel automaton types. This initial population was the seed (i.e. Generation 1 of the population) from which novel automata could be generated.

9.2.1 Generating and characterising the seed population

It was essential that the initial population of automata (at $t = 1$) had the potential to generate new automaton types beyond the initial set of automata whilst also being able to reproduce itself to a degree and thus act as a competitor to novel automata. The following criteria defined the requirements for selecting the automata that would form the initial generation:

1. The selection of automaton types to use in the initial population was guided by the general assumption that - in the most basic self-producing system - self-replication is likely to have preceded the generation of novelty. Self-replicators would have the potential to interact with other self-replicators and therefore had the potential to generate novel automaton types

2. One-state automata were insufficient on their own as a seeding generation as they could not generate automaton types that had more states than themselves. Therefore, at least two automata consisting of two or more states were required (in addition to self-replicating one-state automata) for constituting a viable seed population

3. The initial population should have the minimum complexity required to kick-start the generation of new automaton types whilst simultaneously not introducing any bias into the selection of that seed population

4. The initial population should include interactions that do not generate novelty e.g. self-replication or interactions that re-produce the automata within the seed population. This ensures that the competitive interplay between the re-production of existing automata versus the introduction of novel automata could be examined

The seeding generation of automata that met the above criteria consisted of all one-state and two-state self-replicating automata. The presence of the one-state self-replicating automata satisfied conditions 1 and 3, and the two-state self-replicating automata satisfied conditions 1,2 and 4. The presence of these self-replicating automata ensured that no bias had been introduced into selecting the initial population (which satisfied condition 3). The seeding population was generated from examining the interaction networks for a one-state automata population (G_1) and a two-state automata population (G_2). Those automata that were identified as self-replicators in G_1 and G_2 were added to the initial generation (T_s). The algorithm for generating the seed set is shown in figure 9.1.

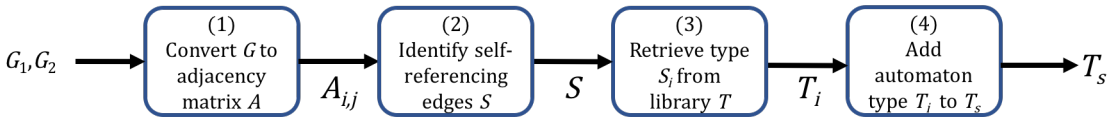


Figure 9.1: The seed population was derived from all one-state and two-state self-replicating automata of which there were 10 one-state and 119 two-state automata for a total seed population of 129 automaton types.

The seed consisted of 10 one-state automata and 119 two-state automata. The average structural complexity was $< C_\mu(T) >= 0.87$ bits and the interaction network complexity was $C_\mu(G) = 12.98$ bits. There were 7,978 closed productions (excluding self-replications) and 5,677 novel productions that generated automata that were outside of the seed set. Figure 9.2 shows the results of simulating the population dynamics of the seed population and where the production of new automata were prohibited. As can be seen the seed population evolved to a steady-state computation niche with no loss of any of its automata. This simulation provided an important insight to the dynamics of the seed population in

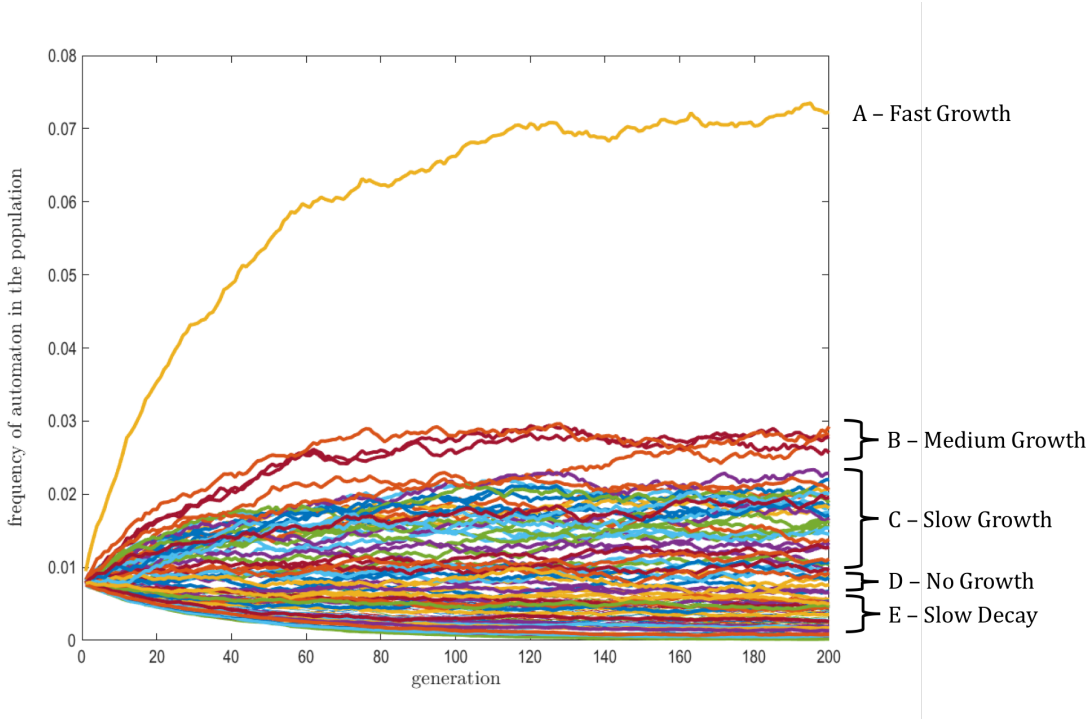


Figure 9.2: The interaction and production dynamics of the seed population over 200 generations where the production of novel automata was prohibited. The seed population had structured itself into four categories of automata: (A) Fast Growth - consisting of a single one-state automaton (S_{10}) that accounted for 7.2% of the population; (B) Medium Growth - consisting of four two-state automata (S_{23},S_{28},S_{35},S_{37}) that collectively accounted for 11.2% of the population; (C) Slow Growth - consisting of 34 automata (four one-state and 30 two-state automata respectively) that accounted for 53.3% of the population; (D) No Growth - consisted of three two-state automata (S_{38},S_{57},S_{94}) occupying 2.5% of the population; and (E) Slow Decay - consisted of the remainder of the seed population with five one-state automata and 82 two-state automata that occupied 25.8% of the population.

the absence of novelty and which provided a baseline for comparing the effect of novelty on this same population.

9.2.2 Setting up the simulation

The simulation was initialised with an average number (775) of each of the 129 automaton types of the seed population which were allowed to interact under well-mixed conditions. Interactions between automata proceeded with the additional step of validating that the new automaton (T_c) satisfied the criteria for an ϵ-machine (see chapter 3 and [126]). Any new automata type (T_c) generated from this process was added to the population by increasing the length of the frequency distribution vector f by $f' =\mid f \mid +1$ to generate a new index $\mid f' \mid$ that became the unique identifier (k) for that automata type in the

population and the membrane. The new automata type (T_k) was added to the set of all automaton types (T) and the interaction that generated that automata type was added to the interaction network ($G_{i,j} = k$) where i, j represented the interacting automata T_a,T_b that produced it. A membrane automaton (M_k) was added to the membrane network and the M_x (incoming) and M_y (outgoing) edges to/from M_k were added according to G_k. This process was repeated for all valid productions of novel automata at time t. The normalised frequency distribution and the edge weightings in the membrane network were re-calculated at the end of the time step and after all valid productions had been completed. The new automata were available to participate in interactions at the next time step ($t+1$) of the simulation subject to their equivalent membrane automata being activated in the membrane (as per the normal operation of the computation niche model).

The population was initialised with the seed automata consisting of 129 self-replicators. The simulation was set to run for 50 generations and the data shown in Table 9.1 was collected at the end of each generational cycle.

9.3 The generation and effect of novelty within a computation niche

Figures 9.3 and 9.4 show the effect of novel automata being generated from an evolving population which initially contained only the seed population. As can be seen the endogenous growth of new types of automata had a significant impact on the seed population with 85 seed automata going extinct (three one-state automata and 82 two-state automata) from the Slow Decay category with only two automata from that group remaining at the 50^{th} generation ($g = 50$).

The normal production dynamics of the seed population had been displaced by the 12^{th} generation where there was a sudden decay in all seed automata (see Table 9.2). The novel automata had grown to occupy 84% of the population by the end of the simulation.

Examination of the population dynamics identified four phases that the population progressed through and these were characterised as Phase I - Diversification, Phase II - Competition, Phase III - Penetration, and Phase IV - Saturation (see Figure 9.5, Figure 9.6 and Figure 9.7):

I. Diversification (generations 1-3). The first transition of the population was dominated by an explosion of new automaton types with 7,322 being introduced in just three generations. This endogenous growth of novel automata immediately displaced the incumbent automata from the initial population which experienced a reduction in their

Data Acquired	Variable	Explanation
Average Structural Complexity	$< C_\mu(T) >$ bits	The internal structure of each automata type was quantified from estimating its structural complexity. The average structural complexity of all automata in each generation provided a quantitative measure of changes within the population
Interaction Network Complexity	$C_\mu(G)$ bits	The interaction network complexity measure provided a quantitative measure of the information required to describe all interactions that could occur and the likelihood with which each production could occur. An interaction network complexity that was increasing could signify two important changes: a population that was becoming increasingly diverse and/or a population that was becoming increasingly uniform
Changes in frequency distribution	f	The proportion of each automata type in the population was captured at each time step which revealed whether an automata type was increasing or decreasing in number
Min, Max, Mean and Standard Deviation	$min(Q)$, $max(Q)$, $mean(Q)$, $std(Q)$	The statistical profile of each generation was examined: automata with the least number of states ($min(Q)$), the most number of states ($max(Q)$), the average number of states ($mean(Q)$) and the standard deviation of the states of automata in the population as a whole. This provided a general indication of the composition of the population at that time
Number of automaton types	$\mid T \mid$	A count of all unique automaton types in the population at time t

Table 9.1: The list of quantitative measurements that were used to characterise the endogenous growth of novel automata from a seed population.

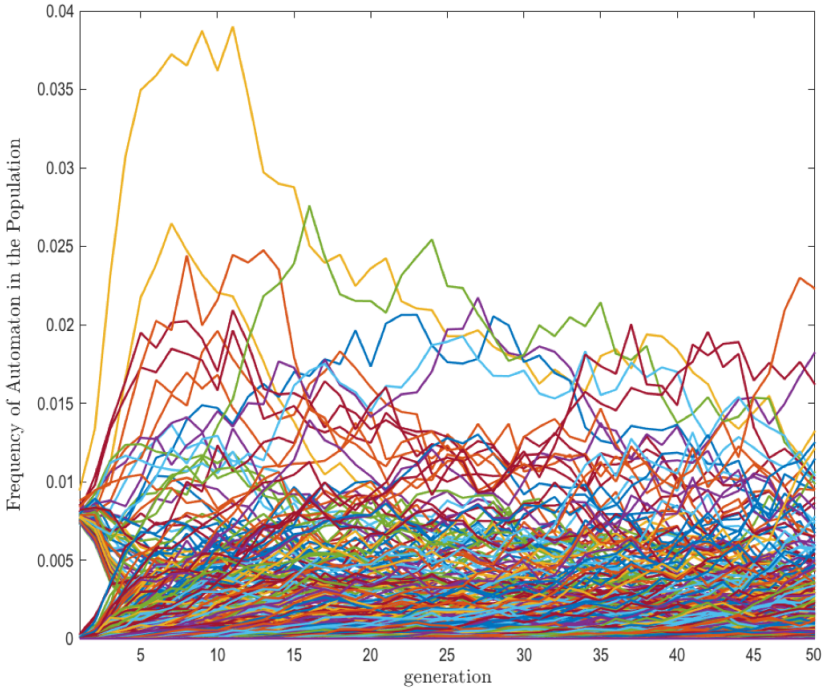


Figure 9.3: The results from simulating the population dynamics over 50 generations leading to the introduction of new (novel) automata that displaced the seed population. As can be seen the seed population decays after the 12^{th} generation due to the significant diversification of the population through the introduction of novel automaton types.

concentration in the population. The interaction network grew in size with 7,732 new vertices added. This was accompanied by a moderate increase in the interaction network complexity (from 13.25 to 13.77 bits) and a significant increase in the average structural complexity of the population (from 1.38 bits to 1.93 bits) - see Figure 9.5a. Even though this phase was the shortest it experienced the most significant rate of introduction of new automaton types of all the phases - see Figure 9.5b.

II. Competition (generations 4-8). The second transition was characterised with increased competition between the incumbent automata and novel automata. The recently introduced automaton types were establishing themselves in the population and increased the range and number of their interactions with other automata. This displaced more of the incumbent automata which saw their relative proportions decrease over this period. The formation of new edges between existing automaton types in the interaction network proceeded at a faster rate than the introduction of novel automaton types (see the sharp reduction in the rate of change that was occurring to the population as illustrated in Figure 9.6). This introduced more structure into the population. This led to greater certainty

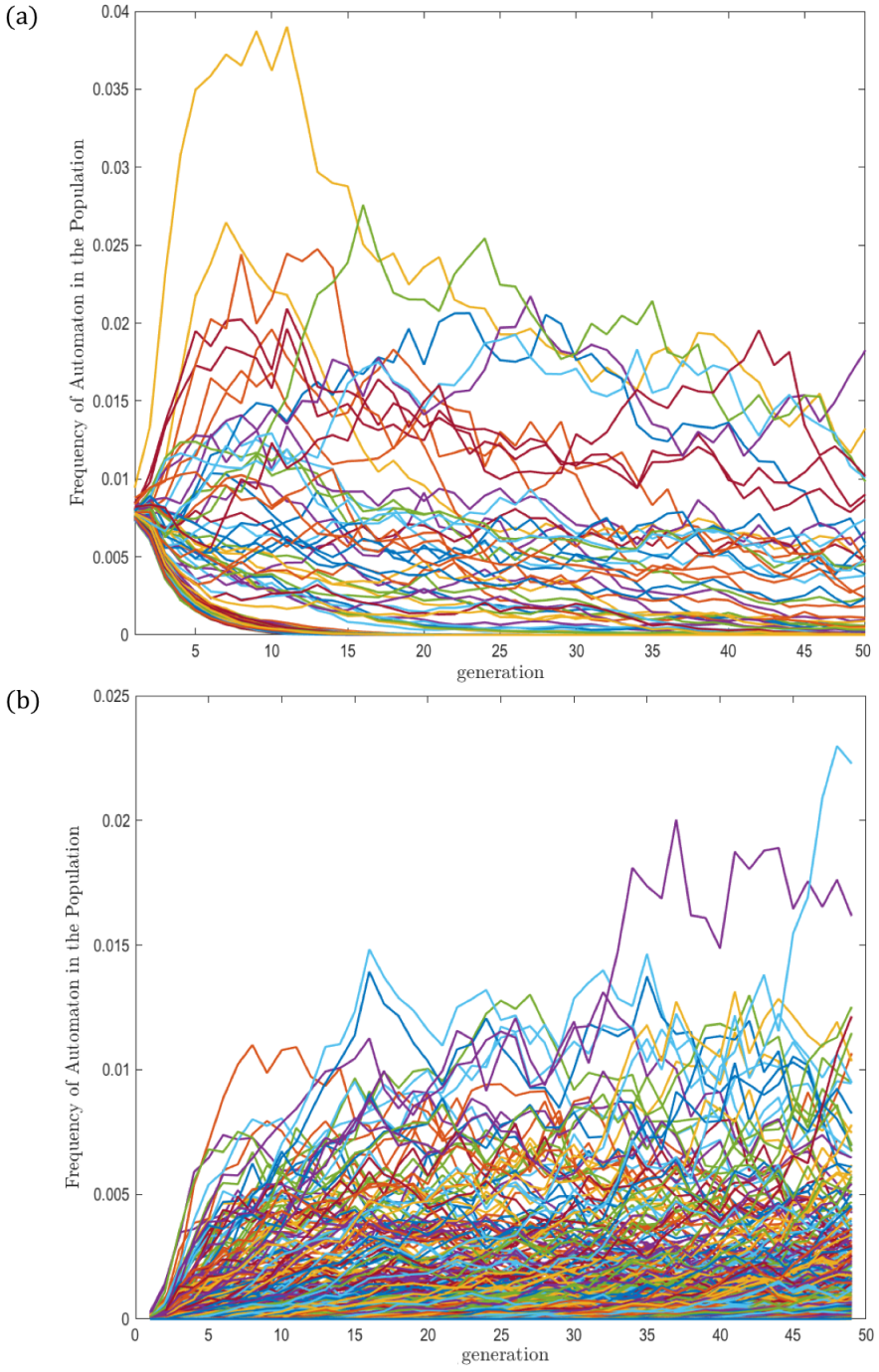


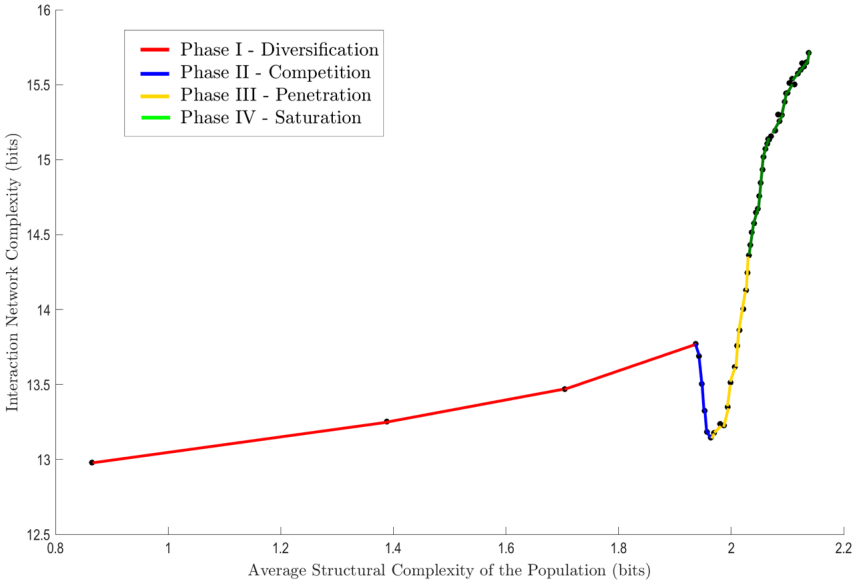
Figure 9.4: The population dynamics over 50 generations isolated to: (a) the dynamics of the seed population only (the novel automata dynamics have been omitted) showing the rapid decay of seed automata by the 12^{th} generation; and (b) the dynamics of the novel automata only which appeared from generation 1 showing growth and diversification as the simulation progressed.

that the next automaton to be produced would come from existing automaton types rather than the generation of a new type of automaton. The reduction in the interaction network complexity from 13.69 to 13.15 bits (see Figure 9.5a) supported this observation. As the majority of productions were of existing automata this led to a significant decline in the rate at which novel automata were being introduced e.g. 570 novel automata introduced over five generations compared to the previous phase of 7,322 novel automata within just three generations - see Table 9.3 for more information on the rate at which novel automata were introduced in each phase and see Table 9.4 for the changes in the interaction network complexity ($C_\mu(G)$) across the phases.

III. Penetration (generations 9-22). The third transition was defined by the continued growth and establishment of existing automata that increased their concentration in the population. The continued rise in frequency of these automata, with the simultaneous decrease in the frequency of the seed automata, introduced more uniformity into the distribution of automata within the population. This was commensurate with the sharp increase in the interaction network complexity from 13.18 to 14.51 bits. This internal consolidation of existing automata was also supported by a significant reduction in the rate of at which novel automata were being produced over this period (an average of 72 new automata per generation).

IV. Saturation (generations 23-50). The final phase was characterised by the rate of change in the population reducing significantly. This phase was similar to the previous phase - increased penetration and consolidation within the existing population at the expense of new automata being introduced - except that the inter-generational changes were significantly fewer. For example, the production rate of novel automata had reduced from 72 per generation (in Phase III) to just 42 per generation in this phase. The rate of change within the interaction network had also reduced as fewer new automaton types were being added to the population. Indeed, the change in the interaction network complexity (from 14.57 to 15.71 bits) saw a significant slow down with an increase of just 0.04 bits per generation in this phase compared to 0.17, 0.1 and 0.07 bits for the phases I-III respectively.

(a)



(b)

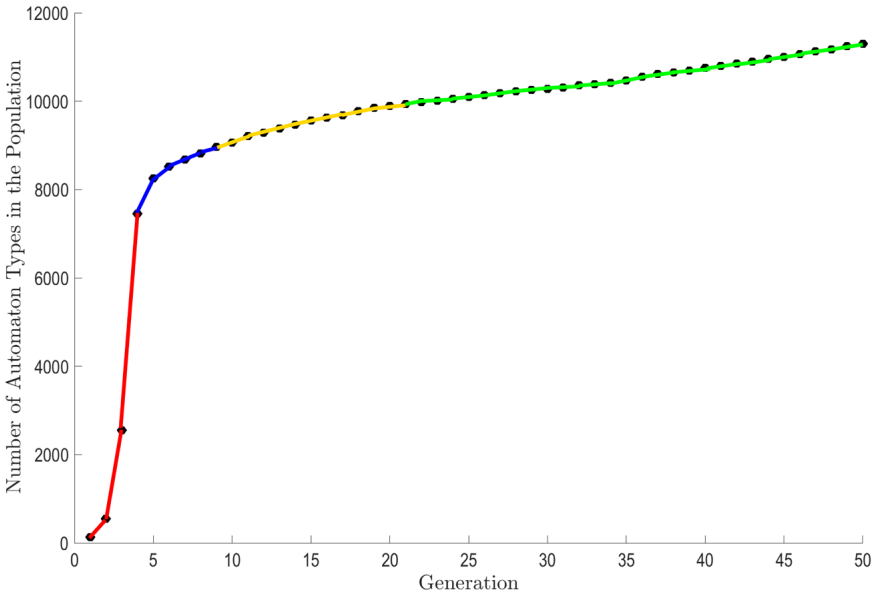


Figure 9.5: Changes in the population over 50 generations could be classified into four distinct phases I - Diversification, II - Competition, III - Penetration and IV - Saturation : (a) the Interaction Network Complexity ($C_\mu(G)$) vs. the Average Structural Complexity of the Population ($< C_\mu(T) >$) over 50 generations; (b) the Number of automaton types in the population at the end of each generation.

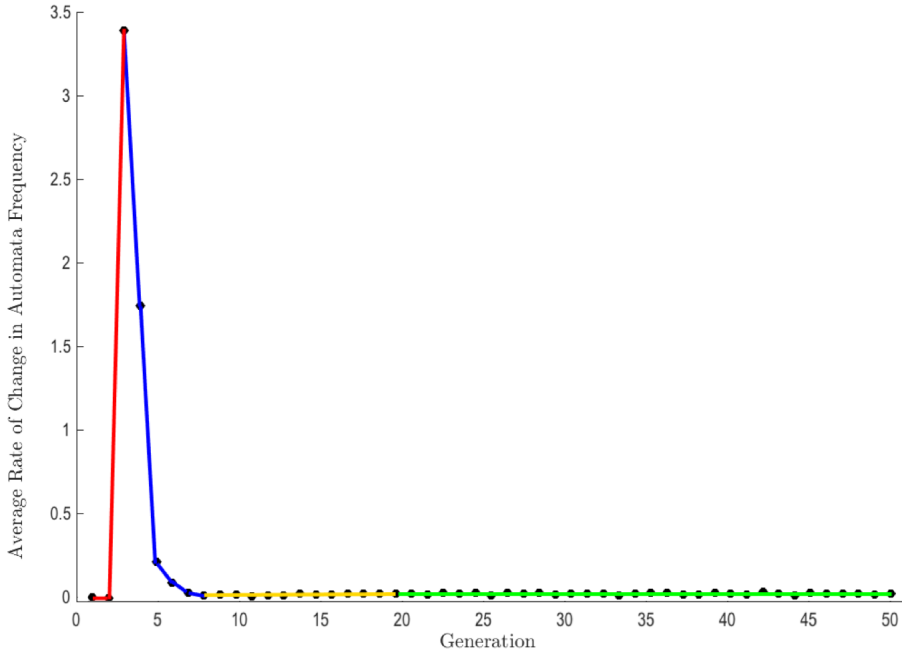


Figure 9.6: The average rate of change in automata frequency in the population indicating that an initial and significant re-structuring of the population (Phase I shown in red) was followed by a drastic reduction (Phase II shown in blue) and levelling off of the rate of novelty and the emergence of a steadier and more incremental introduction of novel automata (Phase III and IV in yellow and green respectively).

Original Category	f at $g = 50$ with Seed Automata Only	f at $g = 50$ with Novel Automata
A - Fast Growth	7.2%	1.32%
B - Medium Growth	11.2%	2.36%
C - Slow Growth	53.5%	11.65%
D - No Growth	2.5%	0.6%
E - Slow Decay	25.8%	0.0006 %

Table 9.2: Comparison of the seed population at the end of 50 generations *in the absence* of the generation of novel automata vs. the seed population in the presence of novel automata. The structure of the seed population was disrupted leading to a significant reduction in the number of seed automata down to just 15.93% and the extinction of 82 of the 129 automata that were originally present at $t = 0$.

Phase	Generation	No. of Types *(change)*	Average Rate of Change
I. Diversification	1-3	129 to 7,451 *(7,322)*	2,440/gen
II. Competition	4-8	8,253 to 8,823 *(570)*	114/gen
III. Penetration	9-22	8,968 to 9,977 *(1,009)*	72/gen
IV. Saturation	23-50	10,010 to 11,302 *(1,292)*	46/gen

Table 9.3: Comparison of the composition of the population by the number of unique types and the rate at which new automata were being introduced within each phase.

Phase	Generation	$C_\mu(G)$ *(change)*	Rate of Change in $C_\mu(G)$ per Generation
I. Diversification	1-3	13.25 to 13.77 *(0.52)*	0.17 bits/gen
II. Competition	4-8	13.69 to 13.15 *(-0.54)*	0.1 bits/gen
III. Penetration	9-22	13.18 to 14.51 *(1.33)*	0.09 bits/gen
IV. Saturation	23-50	14.57 to 15.71 *(1.14)*	0.04 bits/gen

Table 9.4: Comparison of the Interaction Network Complexity ($C_\mu(G)$) and how much it changed (Rate of Change) across the four phases of the population.

Phase	Generation	Average $C_\mu(T)$ *(change)*	Q_{min}	Q_{max}	Q_{mean}
I. Diversification	1-3	1.38 to 1.93 *(0.55)*	1	8	3.75
II. Competition	4-8	1.94 to 1.96 *(0.02)*	1	12	4.5
III. Penetration	9-22	1.97 to 2.03 *(0.06)*	1	17	4.8
IV. Saturation	23-50	2.04 to 2.13 *(0.09)*	1	34	5.3

Table 9.5: Comparison of the average Structural Complexity of the population $C_\mu(T)$ and the automata with the least number of states (Q_{min}), the maximum number of states (Q_{max}) and the mean number of states (Q_{mean}) in the population for each of the four phases. The change in the structural complexity of the population is shown in brackets and was the difference between this phase and the previous phase e.g. the seed population at $t = 0$ had an average structural complexity of $C_\mu = 1.38$ bits compared to the average structural complexity of the population at the end of the 3^{rd} generation with $C_\mu = 1.93$ bits.

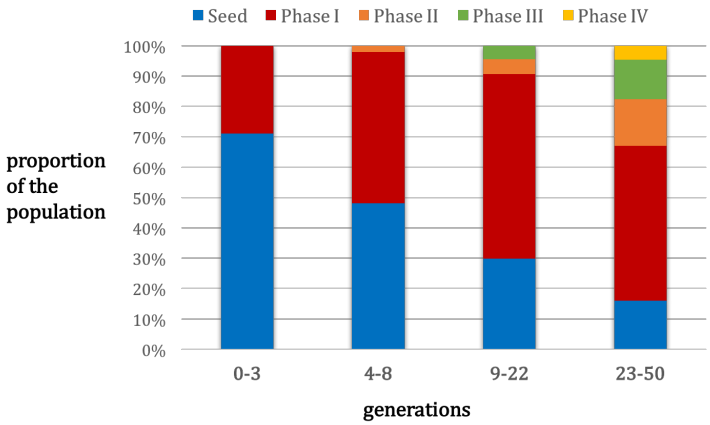


Figure 9.7: A graph comparing the relative concentration of the automata present at certain generations split into the generation in which the automata was introduced to the population. As can be seen the seed population (blue) decayed as the simulation proceeded. The novel automata that were introduced in Phase I (1-3 shown in red) actually increased in number over three generational phases and decayed at a slower rate than the seed population. Subsequent novel automata introduced in Phase II (orange) and Phase III (green) increased in concentration but at a much slower rate than the novel automata introduced in Phase I.

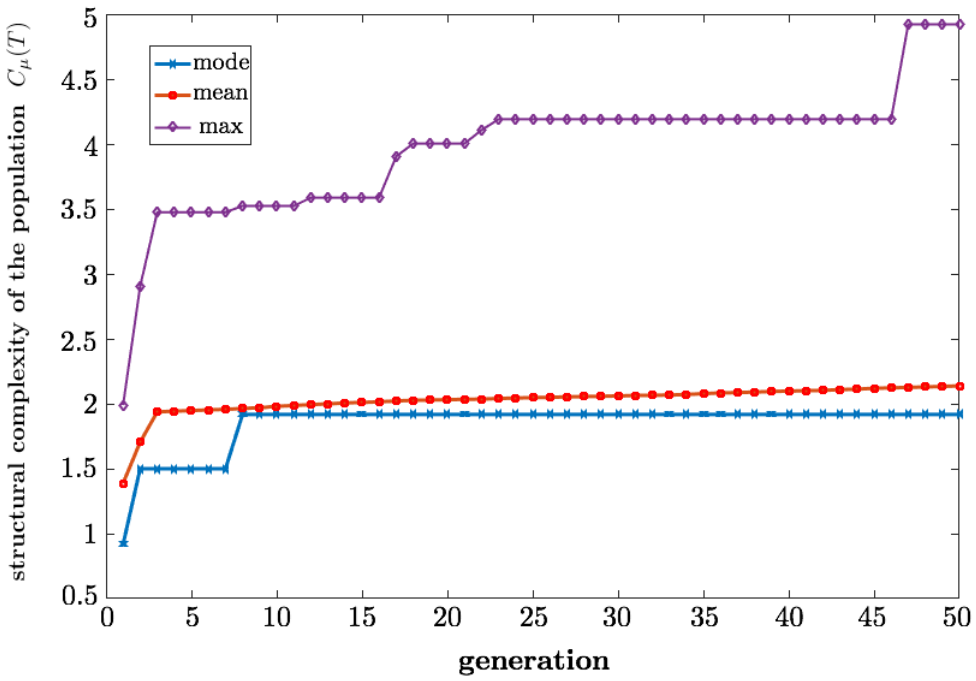


Figure 9.8: Comparison of the mean, mode and the maximum estimates of the structural complexity present in the automata population in each generation.

The interaction network complexity ($C_\mu(G)$) of the seed population at $t = 0$ was 12.98 bits and underwent a very modest reduction to 12.82 bits when dynamics were driven under closed conditions (i.e. novel automata were forbidden) and significantly reduced to 8.33 bits in the presence of increased competition from novel automata being produced and introduced into the population. The average structural complexity ($< C_\mu(T) >$) of the seed population at $t = 0$ was 0.87 bits which was retained under closed conditions and increased to 0.9 bits in the presence of competing novel automata indicating that automata with a lower structural complexity were, on average, less competitive and were more likely to go extinct (see Table 9.5).

Whilst the population was still generating increasingly complex automata throughout the simulation the average structural complexity only incrementally increased whilst the overall mode of the structural complexity of the population was locked in from the 8th generation (see Figure 9.8). These findings were consistent with what would be expected from a 'passive evolution' process [143].

9.4 Summary

This chapter has examined the introduction of novel automata into an existing population. The key findings were:

- An interacting seed population that consisted of 129 self-replicating and network-replicating one-state and two-state automata interacting under the constraint that novel types of automata were forbidden, self-organised into a steady-state organisation structured into five clusters: A - Fast Growth automata (1 off), B - Medium Growth (4 off), C - Slow Growth (34 off), D - No Growth (3 off) and E - Slow Decay (82 off)

- The same simulation was re-run but now with novel automata able to be produced and this resulted in the population failing to self-organise into a distinct, invariant organisation and instead transitioned through four phases: Diversification, Competition, Penetration and Saturation. After an initial explosion of novel automata (the Diversification phase) and within three generations of the population, the growth rate of novel automaton types rapidly plateaued as internal competition came to dominate (the Competition phase) leading to the establishment of novel automata as the dominant types in the population (the Penetration phase) prior to a gradual slowing down of both the level of competition within the population and the rate at which new automaton types were produced (the Saturation phase)

- The initial (seed) population was devastated by the endogenous growth of novel automata and its size was reduced from occupying 100% of the population to just 16% at the 50^{th} generation and with 82 of the original 129 automata going extinct

- Novelty removed any existing structure within the population and, in the presence of continuous novelty, prevented the establishment of any discernible structure. This was demonstrated by comparing the dynamics of the seed population with and without novel automata. In the former a steady-state emerged - a niche - whilst in the latter this ordering of the population was prevented. This was entirely due to the displacement of incumbent automata with novel automata. This was similar to the observed behaviour of a constant influx of automata as seen in the information niche results (see Chapter 4 - 7). Whilst the origin of these disruptive automata was different - an inflow of new automata from an exogenous source compared to the endogenous growth as presented in this chapter - they both demonstrated the

disruptive effect that automata that were not part of an existing interaction network had on the dynamics and structure of the population.

- The disruptive effect of novelty raised questions about the mechanism by which it could be suppressed - possibly through some regulatory feedback mechanism - to allow a steady-state structure of the population to emerge. This highlighted the tension between diversification and consolidation in the population. A system that could intrinsically and periodically move between these two extremes could be demonstrative of a form of organisation that maintains itself in a "window of viability" [144],[52]. A similar observation was made with the reproduction of a niche from the network fragments transferring into a neighbouring population as presented in Chapter 7. The simulation of a system to demonstrate such viable behaviour could be the focus of future work.

CHAPTER 10

DISCUSSION

Chapters 4 - 9 presented the results from simulating the emergence and dynamics of information niches and computation niches under various environmental conditions and perturbations. This chapter summarises those results and evaluates the findings in light of the research questions posed in Chapter 1 and discusses them with reference to related work in the literature.

10.1 Summary of Simulation Results

Chapter 4 presented the results of simulating a population of one-state automata interacting and evolving over a large number of iterations. The emergence of different information niches for various environmental conditions were identified and the information content of each niche was measured. This revealed that the ability for the population to transform its structure in response to environmental perturbations was contingent on its present structure and the nature of the perturbation both of which determined the amount of information within the population at that time. It was shown that the 'fitness landscape' that was sculpted by the environment was not traversable by the population if there was an insufficient amount of information present in the population, and that was required to undergo the necessary structural transformations. This finding is an original contribution to the field of autopoiesis.

This chapter also revealed that there were initially a very large number of production networks that were competing with each other to survive. Such inter-network competition

was in addition to, and related to, inter-automata competition whereby the extinction of an automata type could lead to the collapse of all networks that were dependent on it. Conversely, automata that were produced by several different networks tended to persist due to the inherent redundancy with which they could be produced within the population. Further analysis of these networks revealed that the most competitive networks had four properties: (i) they were strongly connected indicating that each automata type in the network was produced at least once by other automata in the same network; (ii) that when isolated these networks were dynamically stable over time with no loss of any of their constituent automata; (iii) they were hierarchical with larger networks decomposable to irreducible elementary networks which acted as the building blocks for larger networks; and (iv) collectively the surviving networks had redundancy i.e. each automata type in the network could be produced from more than one (and typically several) different networks. These results are comparable to those discovered by Crutchfield & Gornerup [36] whilst there were two new observations from my work: (i) the discovery that the quantified information content of a niche can explain the potential for a population to transform its structure to occupy different niches in the environment; and (ii) the explicit definition of an information niche as a population that transforms itself in response to changing environmental conditions to reach a new steady-state. Crutchfield & Gornerup's equivalent structures were called *meta machines* and whilst this is an accurate description of the composition and relationships of the population (a machine of machines) it does not capture the important observation that different population structures form under different environmental conditions *nor* does it capture the equally important observation that each steady-state structure has a unique measure of information. Referring to these steady-state structures as information niches adds the necessary ecological/evolutionary context required to appreciate the similarities of the dynamics and self-organising behaviour of these systems to biological behaviour. Another closely related work is that of Fontana's algorithmic chemistry which demonstrated similar structures emerging from an initially disordered state. In his work Fontana describes the emergence of Level 0 (self-replication) and Level 1 (networked replication) organisations - with the latter being a self-maintaining organisation - that are equivalent to Crutchfield & Gornerup's ϵ-machine and meta-machines respectively. Fontana's Level 1 organisation is similar to an information niche however, as was the case with the Crutchfield & Gornerup work, there is no explicit consideration of how Level 1 organisations behave under varying environmental conditions. As such, the information niche model offers a more powerful explanatory narrative than either of these two models for how autopoietic systems may form under a range of environmental conditions.

Chapter 5 presented the results for simulating a population of two-state automata

interacting and evolving over a large number of iterations. This led to the emergence of different two-state information niches for various environmental conditions. The two-state automata population was significantly more diverse (1,873 unique automaton types compared to 15 automaton types in a one-state population) and this led to more complex population dynamics with competition now occurring at the automata, network and the niche level. Under well-mixed environmental conditions with automata production driven entirely from endogenous automata the formation of two competing niches emerged and after a period of co-existence an abrupt event occurred that led to the demise of one of the niches. By comparison, in the presence of environmental perturbations those same competing niches were able to co-habit and co-exist within the same space. Finally, under conditions of non-diffusivity and where production of automata was dominated by local interactions only then did two new competing mechanisms emerged that introduced new population dynamics - the 'replicate & lock-in' and 'mutual maintenance' mechanisms (Chapter 6 examined these mechanisms in detail). There does not appear to be any published work that has achieved similar results nor interpretations. The work of Gornerup & Crutchfield [134] examined the population dynamics in an open-ended model where multi-state ϵ-machines could be generated and, whilst that particular work is more related to my work on open-ended novelty (more on this shortly) what is relevant here is that their results do not demonstrate nor do they discuss the emergence of novel forms of competition and competitive strategies between networks of interacting automata. The relationship between an increased level of diversity in the population, and an subsequent increase in the range and type of competitive dynamics that emerge under varying environmental conditions, has been demonstrated here and future work could examine three-state automata populations.

Chapter 6 presented findings on the spatial patterns that emerged on the lattice environment from the one-state and two-state simulations of the information niche model. It was observed that interesting spatial configurations emerged only under environmental conditions of zero mobility of automata (i.e. no diffusive mixing). The one-state niche that emerged under such conditions was characterised as two competing domains of one-state automata separated by a dynamic and continually produced boundary consisting of two other types of automata. This reproduced similar results to unpublished work by Piantadosi & Crutchfield [123] however my explanation of the behaviour of the boundary differs. Piantadosi & Crutchfield have incorporated terminology such as general replicators, spatial replicators and membrane replicators to describe the dynamics observed. Whilst I acknowledge the attraction of categorising the automata in this way I deemed that they were unnecessary and inaccurate. For example, they define a spatial replicator as

an automaton that forms the spatial domains and are 'self-maintaining' which is not accurate. For example, the T_2 and T_4 automaton types that constitute the domains - and in their language are spatial replicators - are not self-maintaining because $T_2 \circ T_2 = \emptyset$ and $T_4 \circ T_4 = \emptyset$. There is no renewal of automata within domains and, in effect, the automata that constitute the interior of a domain have "precipitated" on the lattice. On this basis the notion of a spatial replicator that they have introduced does not concur with what is observed in the mechanics of domain and boundary dynamics. The only dynamic aspect of a domain is at its boundary where domain growth occurs through the outward growth of the boundary which is a function of the interactions between four different automata. Competitive dynamics therefore played out at the immediate interface of domains and boundaries and competition between domains was characterised by the seizure of part of a competing domain through a two-step mechanism of (i) growth of the boundary into a competing domain (as a random occurrence during the continual maintenance of the boundary); and (ii) the replication of the automata from the other domain into the 'hole' left by the boundary automata. This 'protected outgrowth' mechanism proved to be a major survival strategy for the four participating automata with the remaining eleven automaton types going extinct. There is no description or explanation of such competitive dynamics in Piantadosi & Crutchfield's results.

Simulation of a two-state population under low-diffusivity conditions resulted in similar spatial patterns with domains consisting of a single type of automata that had grown outwards until meeting other growing domains. However, there was no evidence of boundary-type automata. Instead the domains were in direct contact with other domains. Examination of the underlying dynamics revealed that two competitive strategies had emerged within the population: (i) a 'mutual maintenance' strategy where a subset of automata were co-operating to continually produce each other at their interface thus maintaining their immediate areas of contact, and (ii) a 'replicate & lock-in' strategy that was significantly more aggressive in outward growth of a domain where in an interaction with other domains these type of automata would only produce themselves. Hence, not only did this allow for the transformation of neighbouring automata into themselves it also meant that there were very few automata that could perform the reverse i.e. interact with one of these self-replicating domains where any new automata that were produced were different from one of the automata that was included in the interaction. This mechanism was termed 'replicate & lock-in' which was a more aggressive form of the 'protected outgrowth' strategy observed in the one-state population. The results and analysis on two-state automata under zero-diffusivity conditions is a new result in the artificial chemistry field.

Chapter 7 simulated two populations - a one-state population and a two-state popu-

lation - interacting either through co-location within the same space or by the transfer of automata from a two-state population into a one-state population. The simulation of a one-state niche ($1A$) and a two-state niche ($2B$) was also performed. The main findings were that: (i) the one-state niche was able to take advantage of the presence of a large number of new automaton types that did not originate from within its own niche and this led to its original automaton types being produced in higher numbers. Indeed, whilst the presence of the two-state automata led to structural changes within the one-state niche, its organisation (and hence its identity) of the one-state niche remained invariant. The two-state niches did not retain their identity; (ii) in the case where the one-state and two-state niches were located in separate environments but with a transfer of automata from the latter into the former, the two-state niche was reproduced in the one-state niche environment. The method of sampling from the two-state automata population (to determine the automata type to be transferred into the one-state population) was effectively re-generating the donating population's structure in the receiving population.

Chapter 8 simulated a one-state computation niche model under a wide range of environmental conditions. With a one-state population the expected structure for a well-mixed environment was reproduced as per the information niche model thus confirming the accuracy and consistency of the results in the presence of a membrane. The membrane had a demonstrable effect on the production dynamics of the internal population which led to changes in the population structure. This, in turn, had an effect on the behaviour of the membrane as the weights on the membrane network were directly correlated to the population structure e.g. the more populous an automata type in the population the higher the weighting on the outgoing edges of its membrane-equivalent automata. However, there was a change in the interaction dynamics of a one-state automata population in the presence of a membrane whereby no automata go extinct. This was examined[1] and was not due - as was first suspected - to the population update occurring synchronously on each time-step rather than asynchronously i.e. any 'activated' automata in the population were deemed to interact on that same time-step whereas in the information niche model only one automaton can be produced per time step. The underlying cause was examined in detail and explained in Appendix 12.3 with the conclusion that the production process in the computation niche model was partially sampling the population (due to the membrane inhibiting some population automaton types) whereas the information niche model was fully sampling the population on each time step. This partial sampling had the effect of boosting the production rate of less competitive automata at the expense of the more competitive

[1]The computation niche model was re-configured to only update one automaton per time-step and several repeated simulations were run under the same conditions as the original simulation.

automata. The consequence of this was that previously poorly performing automata (e.g. T_6,T_9) were retained in the population. This is potentially an important insight to the role of a biological membrane as it suggests that a process for regulating internal reactions improves the survival chances of all constituent components. Such a function increases the ability of the niche (aka. the biological cell) to retain sufficient information that would be required to maintain its identity under a wide range of environmental conditions. This simple insight may aid in our understanding of why compartmented structures tend to be omnipresent in living systems. This warrants further investigation and is recommended for future work.

Another key finding from simulating the computation niche model was that mono-input automata were too simple and were not robust to extreme fluctuations in environmental information leading to their long-term deactivation in the membrane and subsequent dis-engagement of their equivalent automata in the internal population. This was shown to be detrimental to their competitiveness. Emissions from the niche into the environment had the effect of modulating the environmental noise that was subsequently received into the niche via. the membrane. This led to a moderate change in population structure which was demonstrative of structural coupling between a self-producing system and its environment via. an exchange of information.

Chapter 9 examined the effect of the unconstrained production of novel automata starting from a seed population of 129 self-replicating one-state and two-state automata. One-state and two-state self-replicators were chosen as the seed population as they had the ability to reproduce themselves whilst also interacting with each other to generate novel automata. This created a competitive survival pressure where self-replication was competing against novelty generation for occupying the lattice. The generation of novel automata occurred so rapidly that the population underwent significant diversification in just a few generations that the self-replicating automata were quickly displaced. Indeed, there was a runaway effect where too much novelty was introduced into the population and this prevented the establishment of any kind of structure within the population. Eventually the population became saturated with no discernible structure. As such, the conclusion was that novelty destroyed structure when left unregulated, and that this may indicate a critical requirement for any kind of autopoietic system emerging from simple beginnings, namely, an ability to regulate novelty and diversity. In studying this finding the observation was made that there appears to be a 'window of viability' [52],[144] for self-producing systems that were not too simple and not too diverse. The ability for a system to regulate novelty, and therefore the diversity, in its population appears to be an important quality, and this is discussed later in this chapter.

10.2 Evaluation of Results

This project has sought to examine whether autopoietic systems can form from minimal and unstructured beginnings and, if so, the nature of and the properties of such pathways. This has been achieved with the demonstration of the formation of autopoietic systems that occupy a niche within a given environment. These niches persist through a continual process of production (autopoiesis) that assimilates and accommodates (cognition) environmental perturbations through structural transformations. Each of the original research aims will now be evaluated in light of the research findings.

10.2.1 Can autopoietic systems form from simple, unstructured beginnings?

Autopoietic systems that were maintaining a non-physical boundary formed from simple, unstructured beginnings. The formation of so-called proto-autopoietic networks emerged from a highly competitive environment and they exhibited specific properties that yielded a survival advantage. Perturbing these systems revealed a degree of robustness and an ability to maintain the system's identity over time. Maturana & Varela's [7] strict criteria for autopoiesis - that the boundary generated by the network of interactions must be physical[2] - was not completely met by these results. However, given (i) the contested view that systems can be autopoietic if they do not have a physical boundary, and instead are maintaining a non-physical boundary; and (ii) these systems demonstrate an autopoietic process (self-production and an ability to recover from perturbations) and a cognitive process (structurally coupled to an environment) these systems were deemed autopoietic on the condition that they were maintaining a non-physical boundary.

McMullin's heuristic test was passed. In an attempt to make progress on the contested issue of whether an autopoietic system must be maintaining a physical boundary, Barry McMullin's heuristic test [33] states that if a system can maintain its own identity in a shared space with other systems then it can be deemed to be maintaining a non-physical boundary. This test was applied to the results of the simulations on two-state automata populations under the influence of an influx of external, randomly generated automata. Chapter 7 described the long term co-habitation of the same population by competing two-state automata niches without the loss of identity of either. This appeared to satisfy

[2]The continued contestation of whether autopoietic boundaries must be physical remains an ongoing issue within the field.

McMullin's heuristic test, and if we accept that his test is deemed a reasonable indicator of autopoiesis, then we can deduce that these systems were autopoietic.

Spatial patterns emerged under extreme environmental conditions but they were not autopoietic. It is generally held that the formation of a boundary - or a compartment - is a critical step towards increasing biological complexity [145]. Information niches demonstrated non-trivial spatial patterning on the lattice in one-state and two-state automata populations under non-diffusive conditions. In the one-state population, domains and boundaries were clearly evident and maintained by just four one-state automata. These domains were competing and ultimately led to the dominance of one domain leading to a homogenous structure after 10^8 iterations. Boundary formation had occurred directly as a result of a competitive process and led to the success and persistence of the boundary and domain automata co-operating in that process. Compartmentation not only occurred in the most simple system (a one-state population) under a selective pressure but its formation was necessary for the survival and persistence of the entities which had constructed it. This demonstrated a basic autopoietic process in practice. The formation of domain and boundaries confer a significant competitive advantage on those automata that cooperated to form such relationships. The boundary automata acted as an interface between a domain and the rest of the population and, in the simulations, it was seen that the growth of the boundary by encroaching into a neighbouring domain allowed its host domain to grow into the space recently vacated by the boundary. Hence, this protected outgrowth of a domain was an important survival advantage as it reduced the diversity of the population and, subsequently, competition. The spatial patterns formed by boundary and domain automata were reminiscent of those seen in chemical reactions where there is a phase separation of a mixture from one phase into two phases known as spinodal decomposition [146] and the patterns that emerge in reaction diffusion systems exhibiting Turing instability in morphogenetic systems [147]. Models of these systems have taken on a number of different forms [148], such as predator-prey [149], and activator-inhibitor [150] systems. In my simulations the environment acted as a morphogen - an agent (normally a chemical but in this case a change in environmental conditions) - that caused morphogenesis to occur in the population by severely restricting the movement of automata, so that only local interactions were possible. This changed the accessibility that automata had to the full diversity of the population. The resultant competitive automata were those that thrived on local interactions and this was a function of the mutually producing networks that they formed and that were reinforced by the spatial formation of domains and boundaries.

In the two-state population domains were evident however they lacked the dynamic bound-

ary structures evident in the one-state population. Instead the domains were immediately adjacent to each other. Two novel, competing mechanisms (replicate & lock-in, mutual maintenance) emerged through the spontaneous affinity of a subset of automata based on their intrinsic information processing properties. The role of the boundary was important to the growth of a domain in the one-state niche as it translated between two incompatible regions. This effect was missing from a two-state population where domains did form but, in the absence of any boundary-forming automata, the population effectively reached a state of stasis where no domains were able to grow as there were no possible interactions between surrounding domains.

10.2.2 If they exist, what pathways emerged and what were their properties?

Hierarchical, strongly connected networks were a signature feature. A population of automata self-organised into production networks which, in a one-state population, consisted of 7,831 different networks which was reduced to just 29 networks once the population reached a steady-state. Competition between networks proceeded with their constituent members growing or decaying in quantity dependent on the nature of the network itself. For example, networks that were cyclic, redundant, hierarchical and dynamically stable were significantly more competitive than other networks. These highly competitive networks consisted of automata that were more readily produced and formed mutually producing relationships with other similar automata. The importance of cyclical, mutually producing networks itself was not a new result and has been discussed extensively by numerous prominent researchers such as Tibor Ganti [42], Eigen & Schuster [43], and Stuart Kauffman [40] whose work on such networks has been studied in depth by Hordijk & Steel [102],[41]. However, what none of these other works identified - or, at least, explicitly stated - was the quantification of the properties of such competing networks. Neither did they introduce the notion that these networks were competing with other networks and that there were certain qualities which, due to their constituent components, meant that some networks were more competitive than others. For example, Kauffman proposed that autocatalytic networks will arise given enough time and diversity [103] and Eigen & Schuster described what was required for a hypercycle to exist but neither were able to describe what actually emerged under competitive conditions and nor what the properties of those self-organised networks were. However, more recent research on the evolvability of autocatalytic networks [108], complex network formation [151], and measuring the degree of hierarchy in a complex network [152] are recognising the competing

nature of the growth and persistence of such networks. In particular, the proposition that the formation of hierarchical, self-maintaining and enduring networks is a signature component of all biological organisms [153] complements my research findings. Nevertheless, there remains a gap in the literature for addressing the notion that biological networks may have formed from simpler networks that had to compete to survive. Furthermore, a quantitative analysis of the properties of competing networks does not appear to have been explicitly examined within the context of autopoiesis and my contribution here was recently published [50].

The behaviour of 'networks of networks' are claimed to be markedly different to the behaviour of single networks [154] and this rapidly growing area of research has implications for a wide range of subject areas [155]. The characteristics of networks that out-compete other networks has been examined [156] and that measuring the eigenvector centrality of competing networks was an indication of success of that network. Cooperation of networks has also been examined [157]. The examination of the structure of networks in Chapter 4 could be extended to measure the eigenvector centrality of each sub-network. This could be implemented by extending the network detection algorithm (see Section 3.6) to include an estimation of the eigenvector centrality of each network detected. This would simply be a case of calculating the sum of the eigenvector centrality measure of each vertex. If measured for each network these measurements could be used to identify critical dependencies between networks. Such an investigation could form the basis for future work (see Chapter 11).

The information content of a niche. Two measures of information - the Shannon entropy of the frequency distribution of automata and the interaction network complexity - were estimated for each steady-state that the population evolved to. This revealed variations in the amount of information contained within the population at each steady-state and - given the structurally deterministic nature of an autopoietic system - this had a contingent effect on the ability of the population to adapt to changes in the environment. For example, a population in a state that contained low levels of information was not able to "climb" a fitness landscape to states that required higher information content. To do so required an influx of information in the form of randomly added automata from the environment which acted as an exogenous source of diversification of the population. Chapter 4 demonstrated how the full range of environmental conditions (given by c, v, Φ) created a 'fitness' landscape in which the automata population evolved. Each steady-state configuration of the population was called an 'information niche' to denote two factors: (i) that the information required to re-produce each steady-state configuration could be

estimated using Shannon entropy; and (ii) that each steady-state of the population occupied a position in the fitness landscape (a niche) that was created by the environment. In a one-state population six niches were identified. Each information niche could be seen as a 'local optima' [158] within a rugged landscape with the vertical axis representing the production threshold of the population and the population traversing across the landscape in response to changes in environmental conditions. The actual mechanism that drove the transformation of the population from one niche to another was the accessibility of information. For example, in a well-mixed environment with some influx of external automata from the environment all possible automata interactions for a one-state population were possible. The diversity and proximity of the population under such conditions resulted in an ergodic process of production where all possible productions were examined given a sufficient amount of time (this is one reason why the simulations were run for a minimum of 10^6 iterations). Given that a more diverse population required more information then the production threshold to reproduce that population would be higher. Hence, a rate of influx of automata from the environment was promoting information generation in the niche. By comparison, a low mobility environment with no influx of external automata severely restricted the accessibility of automata to the full diversity of other automata with which to interact. This resulted in interactions between automata being restricted to those that were locally available only and such a non-ergodic process eventually led to the extinction of the majority of automata from the population. Information within the context of a self-producing system was about the diversity and accessibility of automata for interactions. This bounded the structural transformations that were possible within the population in response to the prevailing environmental conditions. This led to the interesting observation that the population could only evolve to a niche in the environment if it contained at least as much information as was required to describe that new niche. If the population did not have sufficient information to describe that new niche (e.g. the new niche required automaton types that did not already exist in the current population) then additional information could only be generated through some influx of external automata. Hence, the environment created multiple attractors [66] within an information landscape and in which several different forms of autopoietic system (niches) could emerge.

The population consistently and repeatedly evolved to steady-state niches as defined by the environment. A similar initial population evolving under similar environmental conditions would evolve to a steady-state niche that was similar to previous simulation results. Simulation results were highly repeatable indicating that the information and computation niche models were deterministic for the same initial conditions

and with fixed environmental conditions. Any structural variations between simulation runs were a result of the inherent stochasticity of the 'select and replace' mechanism of exchanging existing automata with new automata. The repeatable and consistent pathways that emerged on each simulation indicated the presence of an attractor. The environment defined these attractors of which there were four across the spectrum of environmental conditions in the information niche model. Even when perturbed the structural values of the population of automata (i.e. their respective proportions in the population) stayed close to the attractor values. A dynamical analysis of the information and computation niche model may yield further insight into the nature of these attractors.

The defining features of these self-producing systems were simplicity, diversity and robustness. Chapter 8 demonstrated the effect of environmental noise on the behaviour of the membrane. Examination of the behaviour of membrane automata showed that those automata that could only process a single symbol (e.g. mono input automaton types) were more sensitive to changes in environmental noise. This sensitivity was particularly acute where the environmental noise was at a constant value and, in some cases, this led to the long-term deactivation of some membrane automata with a subsequent catastrophic impact on their equivalent automata type in the population. Random noise tended to have the effect of maximising the activity of the membrane automata over successive time steps. This observation suggests that there was a minimum level of complexity at which robustness to environmental noise became effective. In the case of an automata population this level of complexity was met when all states of an automaton could process both '0' and '1' symbols. Of course, the intensity of environmental noise (which increased as $\Phi_{in} \rightarrow 1$) would convey the degree of causal influence of those symbols on the information processing that occurred in each membrane automata and which, subsequently, determined whether its activation threshold had been met.

In a population consisting of one-state and two-state automata, and where multiple niches had the potential to form, the niches that consisted of simpler automata (e.g. one-state) were able to maintain their identity and structure whereas more complex niches (e.g. two-state) were not able to maintain their identities. This was due to the production advantage that lower complexity automata benefit from as interactions between automata tended to produce lower complexity automata more often. This advantage was driven by the requirement for new automata to meet the strict criteria of an ϵ-machine and this had quite a drastic effect on reducing the number of states of newly produced automata. This observation aligns with the idea that the most dominant species in evolutionary history happen to be the smallest [159]. Conversely, it also appears to diverge from the generally

held view that evolution moves from simple to more complex organisms [160] but this would be incorrect. Simpler automata, whilst they tended to dominate diverse, multi-state populations, did not drive out all other types of automata. In fact, it was observed that two-state automata were being reproduced and sustained in a population dominated by one-state automata partly because one-state automata interactions were contributing to their production.

The membrane automata had an important modulating and buffering effect between the environment and the population automata. The modulation of environmental noise caused by information emitted from the membrane altered the noise that was subsequently received from the environment. The buffering effect of the membrane minimised the impact on the interactions between population automata when environmental noise was present. Instead the membrane automata processed the environmental noise and whilst this could lead to changes in the production dynamics of population automata it did not interfere with the interactions between those automata. The effect that the environment had on the population was therefore indirect where environmental noise could deactivate membrane automata which in turn inhibited their equivalent population automata from interacting. Environmental noise did not directly affect the interaction network of the internal population. The effect of the membrane on the population was starkly illustrated on the rare occasion where the membrane entered a state of complete de-activation which, in the absence of environmental noise, became a permanent state leading to the death of the niche entirely. It is interesting to note that the environment was the only information source that could re-activate a non-active membrane. The ability for a relationship between the membrane and the internal population to delimit the processes that make up an autopoietic system has previously been refuted by Virgo et al. [16] and instead they have proposed the concept of 'extended autopoiesis'. The emergent roles of the environment, the membrane (boundary) and the internal population that I have observed in the computation niche supports the extended autopoiesis argument. Indeed, the 'operational limits' of the computation niche has to include processes in the environment (in this case the generation and transmission of information to the autopoietic system) to ensure the long-term survival and robustness of a self-producing population.

10.2.3 If they exist, why and how do these pathways form?

Competition was a fundamental mechanism that occurred at multiple levels. Pathways to a self-producing system proceeded through competition between automata leading to "fitter" entities being produced more often, thus ensuring their survival. The

environment defined the fitness landscape which could promote or suppress certain types of automata and networks depending on their fit to the landscape. The critical mechanism driving the emergence of the underlying networks of production was competition between interacting automata to survive in their constrained environment which, as the population evolved, extended to competition between networks and eventually between different niches. Those automata that, by virtue of their composition and interactive behaviour, formed mutually producing relationships with other automata benefited from a collective ability to endure. Redundancy within such networks ensured a degree of robustness to environmental perturbations. None of these properties were 'designed in' nor present under the initial conditions. Chapters 4 and 7 concluded that simpler automata were more readily produced compared to more complex automata. The reason is straightforward: the likelihood of two highly complex automata interacting to produce an automaton of at least the same complexity was much less likely to happen than two simpler automata interacting to produce another automaton of similar complexity. As explained previously this was due to all new automata required to meet the criteria for an ϵ-machine, which involved the minimisation of newly produced automata. Newly produced automata that were very complex were less likely to stay in the same form after minimisation compared to automata that were already of a very low complexity. For example, a one-state automaton could not be minimised and hence would stay as a one-state automaton whereas a multi-state automaton had a chance of being minimised to one consisting of fewer states. Or, to put it another way, there were more interactions that produced simpler automata than there were producing more complex automata. To compound this issue, the lack of more complex automata further reduced the chances of other automata of a similar complexity being reproduced. As such, being a simple form of automata conferred a significant survival advantage through a higher rate of production compared to more complex automata. This finding confirms similar findings in Gornerup & Crutchfield [134] and is analogous to empirical evidence from the real world with the domination of prokaryotes [159].

More complex automata populations generated more complex competitive dynamics. For example, in a well-mixed two-state population two competing networks of automata emerged and it was only through chance that one of those networks came to dominate the population. This repeatable occurrence of two niches competing and eventually leading to the demise of one of those niches had an analog in ecology with the competitive exclusion principle [51].

The membrane was a noisy environment with intrinsic (information transfer between membrane automata) and extrinsic (incoming environmental information) sources of information competing to activate membrane automata. This represented a form of competition

in the membrane whereby information sources (emitting membrane automata) were seeking to maximise their "signal-to-noise" ratio. Each membrane automata was an information source that could transmit to other membrane automata. The receiving membrane automata could accept some or all of the information that the source automata could emit. In a one-state automata population, the membrane network was highly connected with each membrane automata having at least nine incoming edges (receiving channels). These multiple information sources were integrated into a single two-point probability distribution, that potentially activated the receiving automata. The integration of incoming information was a competition between the various information sources, with weak incoming signals[3] unlikely to have a significant effect on the activation of the receiving automata. Concurrently, each membrane automata was also receiving information from the environment. Environmental noise could amplify or dampen signals received from membrane-bound information sources. This implies that an information source that was more effective in activating other membrane automata should receive a benefit from doing so. This may be manifested as: (i) its equivalent population automata getting produced in the population from interactions involving automata of the same type as the activated membrane automata; and/or (ii) receiving information from the automata it activated thus increasing its own chances of being activated in the future. This kind of analysis of the dynamics of the membrane network as information that is transferred, processed and modified lends itself to network information theory [161], which was developed to quantify and understand systems where there were multiple, concurrent information sources and receivers. The use of network information theory to the study of the computation niche membrane dynamics is recommended for future work.

Environmental noise had a significant effect on the activity of membrane automata, which tended to be to the benefit of automata that had more computational capacity as they could process '0' and '1' symbols (dual input automata) compared to just one or other (mono input automata). The environment (as an extrinsic information source) was competing with intrinsic noise in the membrane whilst simultaneously emissions from the niche was modulating environmental information. The noisy environment of the membrane - with automata activating and transmitting simultaneously and that led to changes in the production of new automata - has an interesting analogy to gene expression noise and the effect it has on cellular behaviour [162], [163]. The quantification of gene expression noise

[3] As an example consider an outgoing edge with a low weighting value from a membrane automata sending binary information that was marginal when compared to all other symbols when received at a receiving automaton's input e.g. a '0' was emitted when all other competing channels were emitting a '1' meaning that this automaton's emissions were less likely to influence the activation of the receiving automaton.

in those models treated the total noise as the sum of the intrinsic (membrane) and extrinsic (environment) noise which was consistent with how this was handled in the computation niche.

The environment had a two fold effect on the competitive process in the niche. The first factor - the global parameters c, v, Φ - had a significant effect on the competitiveness of individual automata and production networks as all automata were effected simultaneously. For example, the automata that were highly successful in a well-mixed environment were not at all as effective in a zero-diffusion environment. The environment effectively created a fitness landscape [158] which via. competition within the niche, led to the population transforming its structure until a new steady-state was reached. The second factor - environmental noise affecting the operation of membrane automata - had a dramatic effect on the flow of information within the membrane which subsequently effected the production of automata by promoting the production of automata that had a higher information processing capacity.

In some instances the environment acted to stabilise population dynamics by introducing variation into the population that had the effect of reducing the rate of production of highly competitive automata networks. For example, the co-existence of two two-state competing networks was only present when there was an influx of randomly generated automata from the environment that disrupted production dynamics. This interesting observation - of a stochastic process (the environment) having a stabilising effect on a population and that allowed for the co-existence of competing entities [164] - has been observed in population growth models [165], ecological niches [166], and climate change studies [167]. Indeed, the theory of coexistence [168] has shown that, "environmental variation can buffer inferior competitors against the competitive exclusion principle" [51].

The environment triggered changes in the population. Chapters 4 and 5 showed the effect of the environment on the behaviour of a population of automata. The simulations examined population dynamics under fixed and intermittent conditions and with and without disturbances in the form of material or information influx. The population progressed through a fitness landscape by structural transformations resulting from changes in the underlying production dynamics of automata. The production dynamics were driven by the interaction network and the current concentration of each automata type in the population. This combination determined the probability with which each automata type could be produced. The environment conditions affected these probabilities in three ways: (i) inhibition (or not) of interactions due to restriction of movement of automata; (ii) inhibition or amplification of interactions due to signalling changes from the membrane; and (iii) the

introduction of new automata from exogenous (environment) or endogenous (construction of novel automata) sources.

Under fixed environmental conditions in the information niche model, the simpler the automata (as measured by a low structural complexity) the easier it was to reproduce. Conversely, the chances of reproducing a more complex automata (of higher structural complexity) were less. This was due to the requirement for all newly produced automata to meet the criteria for an ϵ-machine - a minimal representation of a unique information processing function. All new automata were subject to minimisation and, for automata of a higher complexity, this tended to result in a reduction in their number of states. It may be that the chances that this minimised automata would be of the same structural complexity as one of the automata that produced it became less probable as the structural complexity increased. For this reason, complex automata were less competitive when they co-existed with simpler automata. They were not produced as often - which meant that simpler automata were being produced instead - and this exacerbated the situation as the automata chosen to interact were more likely to be of a simpler type. Changes to the environment that affected the mobility and the influx of new automata did not appear to change this relationship. However, in the computation niche model, under intermittent and fluctuating environmental noise, the more complex automata in the population faired better as they had the greater information processing capacity required to handle all binary information.

In general, environmental conditions and environmental noise led to different effects in the information niche and computation niche models. The environmental conditions of the information niche model had a global effect on all population automata by:

(i) impacting on the availability of automata to interact with each other due to changes in diffusivity (as set by the parameters c, υ) of automata on the lattice

(ii) by acting as an exogenous source of diversification of the population by an influx of automata from outside the population (as set by (Φ)

The environmental noise in the computation niche model had a local effect on membrane automata by:

(iii) directly influencing the activation of membrane automata, which indirectly effected interactions between automata, leading to changes in population structure

(iv) preventing a 'dead' membrane state from occurring

The possibility of combining global environmental conditions with localised environmental noise into a single model is a potential area for future work.

Computing the attractor in the environment. A population of interacting automata continually re-produced itself through interactions with other automata in the population. The basis of this interaction was a successful functional composition requiring the output an automata to be compatible with the input of a receiving automata. The new automata then displaced incumbent automata. Given that automata represented a unique function - it transformed the information it received by mapping an input to an output - the growth or decay in the quantity of those functions in the population was an indication of how 'fit' those functions were to the current environment. As the population evolved all possible functions and organisations of those functions were explored - the underlying model and algorithm represented an ergodic process - and the resultant steady-state structure of the population represented the "solution" (niche) that was the best fit of the population to the environment (the niche). In other words, a population of interacting automata computed the attractor in a given environment through a de-centralised and concurrent process of reproducing fitter information processing functions.

The composition and structure of each steady-state population was measured by the Shannon entropy of the number and type of automata. Measuring each population in this way revealed that in some cases the population was unable to traverse the fitness landscape where the information required to describe the population at a different niche was not contained in the population and nor was new information being added from the environment. Information was therefore a measure of the complexity of each steady-state population across a range of environmental conditions.

The information niche could therefore be seen holistically as an integrating function that computes multiple information sources simultaneously (see Figure 10.1). The circular logic depicted in this diagram is reminiscent of the model of a minimal autopoietic system [6], the system logic of a protocell [2] and the logic of social autopoiesis [18].

Complexity begets complexity. The computation niche simulations demonstrated that emissions from the niche had the effect of reducing the Shannon entropy of the environment and that the degree to which it did this was a function of the rate of out flux of information from the niche Φ_{out}. The reduction in entropy of the environment due to modulation with niche emissions was found to be maximal with $\Phi_{out} \approx 0.75$ which resembled a normal probability distribution profile. Above this value and the normal distribution profile began to flatten thus increasing the Shannon entropy. Conversely, the environment

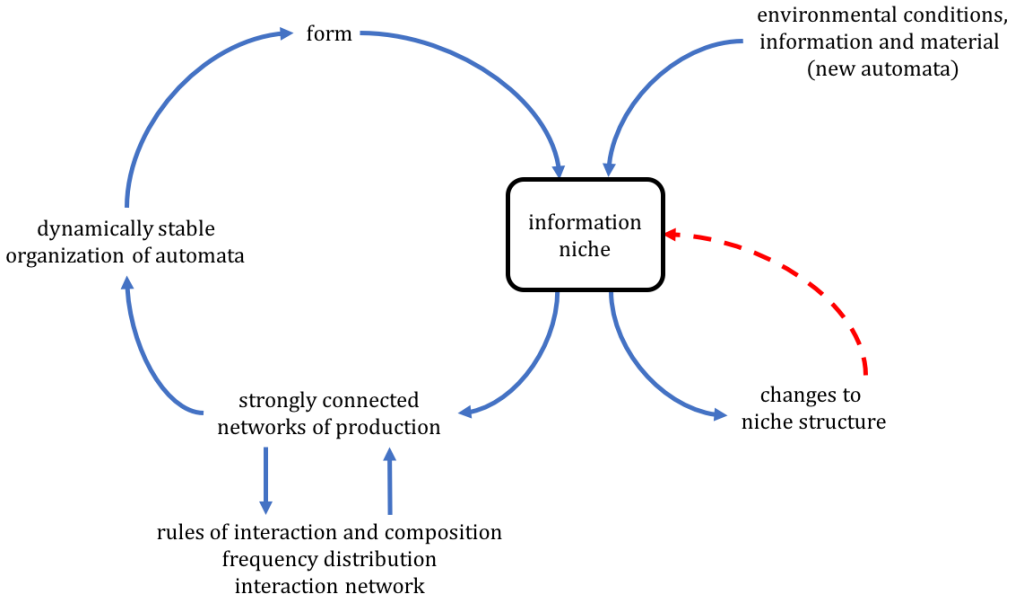


Figure 10.1: The information niche continually integrated external factors such as changes in environmental conditions, information and externally generated automata with internal changes in the structure of its internal population. Taken from [50].

had a marginal effect on the complexity of the niche. This was consistent with Ashby's Law of Requisite Variety [169] which states that the regulatory mechanism of a system must be at least as complex as the system it was regulating and "... the larger the variety of actions available to control a system, the larger the variety of perturbations it is able to compensate [for]" and "... the greater the variety within a system, the greater its ability to reduce variety in its environment through regulation" [169]. The need for operational closure of an autopoietic system required a system to be sufficiently complex to achieve closure but only from the integrated nature of its constituent parts (its unity). If the environment was significantly increasing the complexity of the niche then this would indicate the absence of any operational closure of the system and would be more indicative of an allopoietic system where the processes in the environment were partly, if not wholly, producing and regulating the behaviour of the niche [90]. The Shannon entropy of the membrane was increased when environmental noise was present. Conversely, the environment's Shannon entropy was reduced when the membrane was emitting information. The relationship between the membrane and the environment was examined and this showed that whilst the environment did increase the complexity of the membrane's activity it was by a very modest amount (an increase of 2%) on the complexity that was being generated by the membrane itself. In other words, the Shannon entropy of the membrane was generated

primarily by the switching on/off behaviour of its constituent automata. Therefore, the niche was generating more of its own complexity than it was receiving from its environment and Fernandez et al. [140] suggest that this indicates that the system was autopoietic rather than allopoietic.

The rate of novelty needs to be regulated from the outset. The open-ended production simulation described in Chapter 9 demonstrated an explosion in the diversity of the population progressing through four phases: I - Diversification, II - Competition, III - Penetration, IV - Saturation. As the population evolved through these phases the rate at which new types of automata (novel automata) were produced reduced drastically. Examination of the mode of the population's structural complexity across all fifty generations showed that by the 8th generation the mode of the population was locked in at 1.92 bits and this was characteristic of a 'passive evolution' process [143]. The average structural complexity of the population increased gradually to 2.13 bits and this also concurred with other simulations of passive evolution [170]. There was no clear structure within the population and the interaction network complexity was very high compared to the initial seed population. This was partly understandable due to the significant diversity of the population however it was more than that. The majority of automata were of a very similar frequency in the population (concentration) and this uniformity meant that competition was very intense in the population. Such 'saturation' of the population has been proposed as one reason why dinosaurs went extinct [171].

There was a significant decline in the seed population with a consequent growth in the number of new automaton types. The niche that the seed population would ordinarily evolve to did not get reproduced. The intensity of competition generated from the diverse automaton types created from endogenous novelty rapidly displaced the generations of automata that created that diversity. The population may be cycling through generational waves with the rise and fall of the seed population being replaced by a second wave of automata produced entirely through novelty. More research and investigation is required here and this is a potential focus for future work.

Whilst the investigation into open-ended evolution and the production of *de novo* automata revealed interesting findings the model itself was fairly limited in that it only allowed one form of novelty to occur i.e. new automaton types. The model did not, for example, allow for new species of automata to emerge (e.g. those that process a different alphabet other than binary), or changes to the population itself (e.g. growth or reduction in the size of the population). Such changes would be in the form of 'genotype' variation at the automata level and 'phenotype' variation at the population level. At a more fundamental

level the model does not allow the mechanics of the self-producing system to evolve e.g. the rules of interaction, the interacting units themselves and as such the organisation - in the Maturana & Varela [7] sense - of the system.

In summary, the rapid diversification of the population through endogenous production of novel automata prevented any persistent networks of production to form which would have been required for the onset of proto-autopoietic and eventually autopoietic behaviour. This strongly suggests that real-world autopoietic systems must generate and maintain a regulatory mechanism sufficiently early in its lifecycle to limit or prevent runaway diversification of its constituent population.

10.2.4 What contribution does this make to the theory of autopoiesis?

Demonstrates that autopoietic processes can emerge from undefined beginnings. The simulation results demonstrated the fundamental processes of autopoiesis and cognition emerging from the networks of interactions that formed from a simple population of entities that compete at multiple levels to survive. The underlying population of interacting automata increased in structure over time and reached a steady-state. Such stable configurations provided an enduring and resilient state from which more complex populations could form without loss of the underlying networks of production (e.g. Chapter 7 demonstrated that one-state and two-state niches co-existed within the same space). The possibility for increasing the complexity of the underlying networks of production whilst retaining several concurrent autopoietic identities, within the same space, was analogous to Oparin's 'increasing complexity of an autonomous chemical system' [35]. What was not observed was the spontaneous formation of an ideal chemistry of very few components that efficiently produced a minimal autopoietic system. The simulation of the information niche model under conditions of zero diffusivity led to the emergence of a small (four automata) population that was demonstrating spatial pattern formation of domains and boundaries on the lattice. However, this result was deemed to not be autopoietic as the domain automata were not being maintained and the observed behaviour was partly an effect of how the information niche model was designed.

The criteria for a physical boundary is overstated. The contested issue of whether a physical boundary is a necessity for a system to be deemed autopoietic (as per Varela's criteria, see Chapter 2) was not upheld by this research. Indeed, the opposite was observed: co-occurring autopoietic systems that were cohabiting a shared space maintained their separate identities without the need for a physical boundary. This is further evidence in favour of a 'non-physical' interpretation of autopoiesis that was originally pioneered by

Luhmann [18]. The recently introduced notion of "extended autopoiesis" [16] redefines our understanding of the operational limits of an autopoietic system, and states that those processes that may be physically outside of an autopoietic unit but on which it is dependent should be considered part of its organisation.

10.2.5 What contribution does this make to the origin of life?

These research findings are consistent with Oparin's view. Oparin proposed that the origin of life arose through the increase in the complexity of 'autonomous chemical systems' to the point at which they resemble biological behaviour (i.e. a metabolism) [35]. Complexity here is synonymous with order and persistence which has been demonstrated in this work both qualitatively (e.g. the recurring spatial patterns and networks of production) and quantitatively (e.g. the frequency distribution of automata and the information content of a steady-state population using Shannon entropy). As such, this work reinforces Oparin's view in a similar way that Fontana's algorithmic chemistry does with demonstrating the emergence of viable self-producing structures from simple, unstructured beginnings that can provide the springboard for the construction of more complex forms of organisation.

10.2.6 Can autopoietic theory contribute more to evolutionary biology?

Autopoiesis and Darwinian evolutionary processes may exist on the same continuum. Autopoiesis and Darwinian evolution could be complementary in two ways:

(i) Darwinian evolution does not account for the origin of life as, ontologically, it does not set out a description of what a living system actually is; Darwinian evolution is a phenomenological theory based on empirical observations [30]. By comparison, autopoiesis does define what a living system is and, as such, potentially offers an important theoretical basis for Darwinian evolution. Darwinism is dependent on the transfer of information between generations of organisms and this is dependent on templated replication for the processes of variation, heredity and reproduction to occur. However, this is dependent on the presence of sophisticated molecular machinery such as DNA and proteins. What processes may have existed prior to the emergence of such biochemistry? What possible pathways are there from the inception of a living system to the interwoven complexity of the biology which is now referred to as the modern synthesis [172]? This is where autopoiesis has an explanatory power that potentially reaches further back in time and to simpler chemical environments that gave rise to the first living systems. Whilst the concept of autopoiesis has been demonstrated with a toy chemistry consisting of three chemical

entities [6], these approaches assumed the occurrence of an infinitesimally improbable event where an ideal chemistry spontaneously formed and that happened to endure

(ii) competition is the universal mechanism by which the steady-state populations in the information niche and computation niche simulations are formed. Natural selection is also a competitive process. As such, both theories have a common process - competition - that could be understood as extending on a continuum from chemical competition through competing networks to competing autopoietic units and so on to competing species and beyond that to competing ideas and norms in a social context. In this way one could argue that the natural selection process of Darwinian evolution is present even in a minimal, non-genetic system such as the proto-autopoietic populations studied here. The conceptual gap between autopoietic theory and evolutionary theory is therefore arguably non-existent, and instead a continuum on the pathway from simple, competing networks through to abiogenesis and onwards to multicellularity and larger organisms exists, and should be identified as such. The fundamental mechanism that drives this continuum is competition that occurs at multiple levels (individual, network, niche) and as new, emergent properties are formed which themselves contribute to enrich the competitive dynamics. I am not aware of any literature in the field of autopoiesis that has made such a fundamental link between autopoiesis and Darwinian evolution based on the idea that they share a common mechanism - competition - that binds them at a theoretical level

A 'window of viability' exists. The results of the one-state information niche model (chapter 4) and the one-state computation niche model (chapter 8) demonstrated the importance of a system's ability to modulate its interface with its environment. Too little exposure to the environment and the system became too simplified (e.g. the significant reduction in the diversity of the population due to extinction of the majority of automaton types caused by zero mobility environmental conditions) leading to a lack of information, and too much and it was impossible for any kind of system identity to form (e.g. a very high influx of externally generated automata). There was a 'window of viability' [52] [4], a 'Goldilocks zone', of the possible state space (or, the fitness landscape defined by the environment) characterised by more moderate exchanges with the environment. It may be that autopoietic systems happen to be able to efficiently and effectively maintain themselves in this window of viability. Indeed, cognition is the process by which this

[4]The 'window of viability' is a phrase coined by Ulanowicz and colleagues [52] to define a limited state space where a system maximises its sustainability which they show tends to reside where the system is sufficiently diverse whilst simultaneously being sufficiently efficient. Diversity introduces important redundancy into the system thus allowing it to respond to shocks and perturbations from its environment. Efficiency ensures that the system is able to effectively use resources to maintain itself.

could be achieved i.e. accommodation of changes in the environment by alteration of the autopoietic network. Those forms of organisation that are self-producing but not sufficiently cognitive may be less competitive and therefore do not endure. This was seen in Chapter 4 with the finding that there were 7,821 possible networks and yet only 29 persisted. Such competition between networks led to the survival of those networks that supported the production of a plastic structure that could retain its identity under environmental perturbations. The vast majority of networks which could not achieve this - because they were not mutually producing, dynamically stable or strongly connected - did not survive. Furthermore, very simple populations of automata (e.g. one-state) were unable to generate novelty and therefore could not evolve. The presence of multi-state automata (e.g. ≥ two-state) was necessary for the production of novel automata. As such, there is a minimal level of complexity that a population must have, or that it can develop, to allow the production of novelty. Such an ability may be important to how such systems maintain themselves within a 'window of viability'. As has previously been explained, novelty cannot proceed unchecked and the role of a systems interface (a membrane) may be the key to ensure that just the right amount of diversity and level of information is maintained within the population.

Elementary networks are the 'fragments' required for reproduction and heredity. As described in Chapter 4 elementary networks were self-producing, dynamically stable networks that were irreducible (i.e. the removal of one automata type from the network would mean the network ceased to exist). Elementary networks benefit from having the attribute of dynamic stability. As such, under constant environmental conditions these networks were persistent and provided an important foundation for the creation of more complex networks of production thus creating a hierarchy of networks. They were the building blocks of the larger networks that were required to achieve operational closure of the system. It was shown (see Chapter 4) that a one-state niche was re-produced from a 'seed' of just three elementary networks which cooperated to produce two larger, intermediate networks which themselves cooperated to generate the network that produced and maintained the niche. As such, elementary networks were 'packets of information' that were important in the reproduction of a niche as observed in the reproduction of a niche through the randomly selected transfer of individual automata from one niche to another (see Chapter 7). Hence this was a simple demonstration of the reproduction of an autopoietic system that "... takes place whenever a unity ... undergoes a fracture that separates fragments with individual structures realizing the same organization that characterized the original one" [7].

I hypothesise that Maturana's 'organisational fragments' [32] could be elementary networks. Chapter 7 demonstrated that self-producing systems are able to reproduce themselves from 'fragments' of their own organisation. A related idea in the literature is that autocatalytic networks compete and form irreducible 'autocatalytic cores' [106] that act as 'units of evolution' in large molecular networks. However, as discussed by the authors, their work did not specifically address heredity nor autopoiesis.

10.2.7 How can a better understanding of the pathways to autopoiesis assist with the design of protocell experiments?

Signposting possible processes and architectures for pre-Darwinian protocells. Chapter 2 cited that one of the challenges to protocell research was designing experiments whereby a minimal protocell (e.g. a vesicle) can evolve through a series of pre-biotic transitions towards more mature and sophisticated cellular structures. Such 'protocells as units of prebiotic evolution' [63] need to have the capacity to expand and grow in functionality whilst achieving integration of that functionality. One of the challenges for designing experiments is to achieve "far-from-equilibrium chemical assemblies that involve low-molecular-weight species... divide with regularity, [and] explore an ample range of - sufficiently robust - phenotypes, and have potential to set up mechanisms for increasingly reliable heredity" [63]. In more abstract terms, how can very simple entities self-organise into repeatable structures, that are sufficiently robust, to retain their identity and reproduce themselves without loss of that identity? Such an ability has been observed throughout my project. My notion of an information niche, as a dynamically stable strongly connected network of mutually producing entities, that form distinct organisational steady states under various environmental conditions, may provide a guiding framework for experimental researchers.

Designing in competition and diversity. Autopoietic forms of organisation are strongly dependent on the structure of the emergent network which itself is contingent on the diversity of the population and the environmental conditions that are present. It is recommended that experimental researchers consider the system-level relationships between all entities in the design of protocell experiments especially with a view to 'designing in' competition between those entities.

10.3 Summary

This chapter has discussed the results generated during this project with respect to the contribution that this makes to the theory of autopoiesis. This was done through analysis of the research findings and comparison to the literature where appropriate. The progress that this project has made in answering the original research questions have been evaluated and possible candidates for future work have been identified.

CHAPTER 11

CONCLUSION

11.1 Summary of Research Findings

This thesis has sought to answer the question of whether autopoietic systems can emerge from simple, unstructured beginnings. The conclusion is that autopoietic systems do emerge quite readily across a wide range of environmental conditions.

Two computational models were developed to address this question - the information niche model and the computation niche model - which reproduced a population of finite state automata interacting and producing new automata within a finite space coupled to an environment. A wide variety of simulations of the models were run over a large number of iterations under various conditions related to diffusive mixing and the rate of influx of new material and information. The results were analysed using quantitative techniques from information theory (Shannon entropy [48], interaction network complexity [36] and structural complexity [37]) and network theory (graph construction and degree distribution [49]) as described in Chapter 3. The models and all simulations were implemented in MATLAB and performed on a local computer and occasionally on the University of Bristol's supercomputer BlueCrystal. All of the results were analysed for structural changes to the population and characterisation of the underlying networks of production.

Autopoietic systems form from simple, unstructured beginnings. Simulation results consistently demonstrated that an initially uniform and unstructured population evolved to a steady state structure - a niche - that persisted even in the presence of envi-

ronmental perturbations. The processes of autopoiesis and cognition emerged routinely and repeatedly across different simulation runs. The limitation of this result was that a physical boundary was not demonstrated. Historically the criteria for an autopoietic system has prescribed that the boundary created by an autopoietic process must be physical. However, and as discussed in Chapter 2 and 10, there is a growing consensus that an insistence on a physical boundary is too limiting and that non-physical boundaries (e.g. as evidenced by a system that is able to maintain its organisational identity in the presence of environmental changes) also satisfy the boundary criteria.

Operationally closed networks of production emerged. These structured populations were continually produced from a hierarchical, strongly connected and dynamically stable production network that was formed from the interaction affinity that existed between the interacting automata. Such networks were shown to persist based on their ability to produce the components which constituted the network itself. These networks produced all of the components required to continually re-generate the network. These operationally closed systems are the hallmark of an autopoietic system. Such networks formed readily and repeatedly across simulation runs with the exception of extreme environmental conditions that inhibited all interactions and endogenous production within the population.

The environment sculpted the landscape through which a self-producing system transformed itself to occupy a niche. It was evident that the range of environmental conditions that were being simulated were creating a 'fitness landscape' which drove the structural transformation of the population from one steady-state structure to another. Each niche represented a steady-state organisation that was operationally closed and that was structurally coupled to the prevailing conditions of the environment.

The structure of autopoietic systems can be quantified. Quantitative measurements of the steady state structure of the automata population provided an estimate of the information content present in each niche. Comparison of these measurements for one-state and two-state niches revealed one of the main findings of this project: a niche could only transform its own structure to another niche in the environmental landscape if either it (a) already contained enough information, or (b) the changing environmental conditions generated the necessary information required to generate the structure of the destination niche. This is a new result in the field of autopoiesis and has the potential to become a practical approach to quantifying autopoietic structures.

New methods were developed to fully examine the constructive processes that were occurring. To fully explore the nature of the proto-autopoietic networks that emerged and competed two methods were developed: (i) an algorithm to detect strongly connected networks in an evolving population of interacting automata, and (ii) a numerical simulation implementation of a differential equation to determine the dynamic stability of a network. The development of these methods were necessary to identify the properties of the proto-autopoietic networks that emerged.

Elementary networks enable reproduction and heredity. Each niche consisted of a large network of networks that described all possible interactions within the population. These networks were decomposable to elementary networks that were irreducible, dynamically stable and strongly connected. They were the building blocks for the larger networks that were required to achieve operational closure of the autopoietic system. In simulations of the transfer of automata from one niche to another these elementary networks were reproduced in the receiving niche. Once present in the receiving population they ensured the continual production of their constituent parts thus forming a niche within a larger niche. Over time, and as more automaton types were transferred into the receiving niche, more elementary networks were formed which, in turn, began to combine into larger networks. This continued until the autopoietic network that formed the donating niche was reproduced in the receiving niche leading to the reproduction of the entirety of the donating niche in the receiving niche. This demonstrated a basic form of reproduction and heredity of an autopoietic system.

A 'window of viability' exists. The robustness of a niche was contingent on the composition of the population itself. There were two factors to consider: (a) if the population was too simple, both in terms of variety of automaton types and the information processing capacity of those types, then as demonstrated in this work they were ineffective under constant environmental noise and more complex automata were more resilient; and (b) in the absence of any regulatory mechanism the population of automata produced increasingly diverse and increasingly complex automata leading to saturation of the population. A saturated population lacked any structure as the underlying networks of production were diversifying too quickly and too frequently for any kind of recurring pattern of production to emerge. This suggests that there was a 'window of viability', whereby a population was sufficiently diverse such that the processes of autopoiesis and cognition could maintain the system within this window.

11.2 Concluding Statement

An unstructured population of finite state automata self-organise to steady state structures that are maintained by an operationally closed network that has the properties of mutual production, redundancy and dynamic stability. Such properties are required to enable the processes of autopoiesis and cognition and thus continually produce and maintain the population's identity within a changing environment. As these systems transform themselves to new steady-states in the presence of environmental conditions they are called niches. Niches satisfy all of the criteria for autopoiesis on the condition that a non-physical boundary is accepted.

11.3 Limitations of this research

Although this research has achieved its aims there were some unavoidable limitations as follows:

Limited demonstration of co-operation. Co-operation between autopoietic sets has not been demonstrated. Interactions between autopoietic units was examined and this demonstrated the degree of robustness and reproducibility of autopoietic units however the emergence of a critical dependency between two separate systems was not observed e.g. one autopoietic system 'giving up' the ability to produce one or more automata on the grounds that it now received it from a neighbouring autopoietic unit. The structural coupling between autopoietic units remains an active area of interest with potential insights that could contribute to computational studies of multicellularity [173].

Physical accuracy. The information niche and computation models do not accurately reproduce the physical behaviour of chemicals in a confined vessel e.g. the lack of any consideration of thermodynamics and the contingent effect that this may have had on population dynamics. However, this would have increased the sophistication of the model beyond the design priorities that were set out in Chapter 1 which were to determine the minimal number of features and mechanisms required to reproduce the dynamics and emergence arising from interacting populations.

Scalability. The computational cost of searching for all possible interactions within an open-ended model very quickly became prohibitive. For example, in a 3-state automata population there were 1.6 million unique automata representing 2.75×10^{12} possible interactions each of which would need to be examined for the potential for a successful interaction. Furthermore, to ensure the integrity of the population the results of each of

those interactions would need to be minimised and examined for whether they satisfied the criteria for being a valid ϵ-machine. This is computationally prohibitive, and so whilst the prospect of examining a very large range of unique processes and their collective organisation is compelling, this highlights a major constraint on the information niche and computation model.

No validation with experimental work. There was no translation of the insights gained from this research into a framework for designing experiments for the fabrication of bottom up protocell fabrication [4] from simple beginnings. This could have provided an important opportunity to understand the challenges and opportunities from going from *in silico* to *in vitro* research. The opportunity to test and revise the conclusions of this project based on real-world experimental results could have been valuable and should be the focus for future work.

11.4 Recommendations for Future Work

There are a wide range of possible avenues for further investigation into the emergence and evolution of autopoietic systems. I believe that the cultivation and development of the computation niche model - whilst retaining the ethos of making minimal assumptions in the design of a computational model - should continue to yield insights into the nature of self-producing systems. In parallel, I also believe it is important to bridge the gap from computational study to experimental study. On both points I make the following recommendations for future work:

Measure and analyse the information dynamics in a computation niche. As discussed in Chapter 10 the computation niche model can be understood as being composed of connected stochastic processes. The information flow between these processes could be estimated using information-theoretic techniques such as transfer entropy [141] and active information storage [174] to quantify the computation that is occurring within the model. Existing literature [142] provides not only a framework for understanding computation in a complex system but also the open-source software - the Java Information Dynamics Toolkit (JIDT) - required to estimate information flows. Such work may yield an insight to the architecture of the niche, which may yield an insight into hierarchical causation [175] of an autopoietic system captured as bottom up, same level and top down information flows.

Model populations of niches. Second-order autopoietic structures [7] have been suggested as the pathway from single autopoietic units to either meta-autopoietic units (interacting autopoietic systems that retain their own identity) or the integration of two autopoietic units into a unity (so called symbiosis). There are clear parallels here to the major evolutionary transitions [17] from single cells to multicellularity. The emergence of second-order autopoietic structures could be investigated by "coarse-graining" the computation niche model such that each lattice site is occupied by a computation niche. Each computation niche should itself consist of a lattice occupied by individual automata (as per the current computation model). Neighbouring niches should be able to exchange automata and information with each other and their environment. Such a model would match that described by Maturana & Varela [32]. Whilst it is hoped that such a model would demonstrate co-operation between niches care would need to be taken not to 'design in' such a mechanism. From a pragmatic standpoint such a model would benefit from the implementation of parallel computing techniques to handle an inevitable increase in computational cost. Research on the transition to multicellularity/second-order autopoietic structures has received scant attention although it has recently been reported [176] that autopoietic principles have been applied successfully to explain how cells in a multicellular system handle environmental disturbances and self-maintenance.

Incorporate energy considerations into the model. Seminal work by Landauer [177] on the "physics of information" examined the irreversibility and heat loss that occurs from information processing. In essence, the erasure of a bit of information must lead to an increase in entropy with the minimum possible amount of energy required to erase one bit of information - the Landauer limit - given by $kT(ln2)$ where k is the Boltzmann constant, T is temperature and $ln2$ is the natural logarithm of 2. The premise here is that an information processor generates heat (energy loss) as it manipulates information (e.g. receives a 0 and outputs a 1). The addition of an information thermodynamics dimension to the computation niche model would (i) bring the model closer to a more rigorous and physical explanation of the emergence of the dissipative structures on the pathway to autopoietic forms of organisation, and (ii) the energy cost of information processing [177] and information flow [178] could be studied under the general heading of information thermodynamics [179]. The extension of the computation niche model to incorporate an energy representation would allow the information thermodynamics near and at steady-state configurations to be examined. In other words, the information thermodynamics of an autopoietic system could be estimated for the first time. Such a model could also be used to examine dissipation-driven adaptation [180].

11.5 Final Thoughts

Pathways to autopoiesis have been investigated using an abstract model of a population of interacting automata that self-organise to steady-state self-producing structures. These results were highly reproducible and the only occurrences where such structures did not form was under extreme environmental conditions. Characterisation of a niche identified the emergent properties of dynamic stability, hierarchy and strongly-connected networks with inherent redundancy.

The theory of autopoiesis is undergoing something of a resurgence primarily due to increased efforts in synthetic biology and protocell research (where it has been adopted as a general framework for minimal cell architectures) and, more recently, the surge in interest in artificial intelligence and the search for suitable models and architectures for achieving the goal of "embodied AI" [181].

Whatever the future may hold for autopoietic theory a greater understanding of the pathways to their formation and the structures and processes that emerge on that journey can only assist with the application of the theory within and beyond its field of origin.

CHAPTER 12

APPENDIX

12.1 The pragmatics for handling multi-state automata populations

Interactions between automata with more than one state ($|Q| > 1$) can produce new automaton types that have up to $|Q'| = |Q| \times |Q|$ states. Figure 12.1 illustrates the functional composition of two two-state automata. However, the new automaton generated from the functional composition operation (Q'), may not represent a valid ϵ-machine [126] for the following reasons:

1. If one or more states in Q' are not accessible from any other states (a so-called unreachable state) then this Q' is not a valid ϵ-machine
2. If one or more states in Q' do not have an exit transition from that state to other states then this means that the automata is not a strongly connected component and therefore is not a valid ϵ-machine

If either of these conditions are met then Q' is not a valid ϵ-machine. However, it is possible to *minimise* an automata by (a) removing unreachable states (which addresses the first condition); and (b) identifying states that are equivalent (they read and send the same binary information) and combining them into a single state that may help to overcome the second condition. The procedure required to undertake these steps is to minimise the automaton using the Hopcroft algorithm [127]. After these steps are taken the test for a

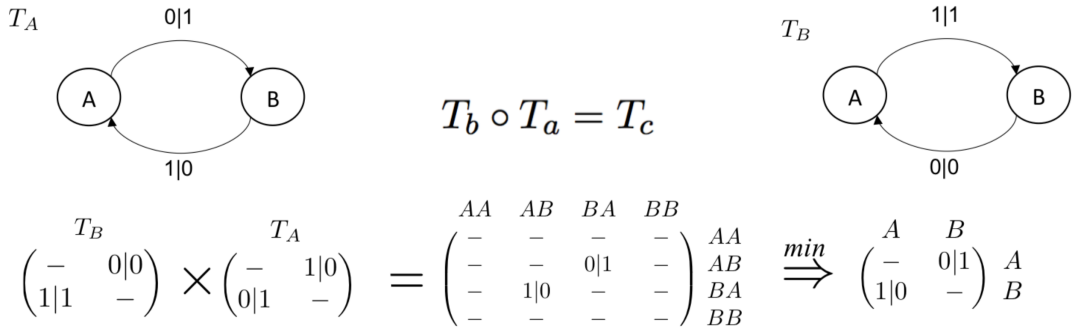


Figure 12.1: Illustrated example of the functional composition of two-state automata (T_a) and the two-state automata (T_b). Each automata can be represented as a 2×2 matrix and the cross product yields a four-state automata T_c. Subsequent minimisation (min) of the product automaton reduces to a two-state automata that represented a valid ϵ-machine. The new automata was identical to T_a indicating that in this interaction T_a successfully replicated itself. Taken from [121].

valid ϵ-machine was re-applied. Those automaton types that were valid ϵ-machines either before or after minimisation were added into the population. If a minimised automata type met either of the above conditions then it could be deemed an invalid automaton type and discarded.

The run-time required to execute the Hopcroft algorithm increased in polynomial time as the complexity of the automaton that was being minimised increased. This raised practical issues with the amount of computational resources required to run the Hopcroft algorithm on multi-state populations. Table 12.1 illustrates the number of interactions that would need to be evaluated (i.e. functional composition followed by minimisation) to construct an interaction network for the population, and subsequently, the estimated total run time required:

Q	$\mid T \mid$	$\mid G \mid$	O($n.s \log n$)	Total Run Time	Cumulative $\mid G \mid$
1	15	225	-	-	225
2	1,873	3.5×10^6	8	2.8×10^7	3.6×10^6
3	1.6×10^6	2.75×10^{12}	19	5.2×10^{13}	2.76×10^{12}

Table 12.1: The Hopcroft algorithm [127] had a worst-case run time of O($n.s \log n$) where s was the size of the alphabet processed by the automata (i.e. 0 | 0, 0 | 1, 1 | 0 and 1 | 1, hence $s = 4$) - and n the number of states of the automata.

As can be seen the computational task involved in processing the interactions between automata with $Q > 2$ states becomes a significant challenge. Two alternative strategies were developed to make the simulation of multi-state automata populations practical: (i) the generation of the interaction network G of a population *a priori* so that it could be used as a lookup table during the simulation of an exclusive two-state population (see

Task	T_b range	T_a range
1	1 to 116	1 to 1873
2	117 to 233	1 to 1873
..	..	..
16	1740 to 1873	1 to 1873

Table 12.2: Constructing the interaction network for a two-state automata population through 16 tasks distributed across 16 compute nodes. Taken from [121].

Section 12.1.1); and (ii) the interaction network was constructed in real-time only for the automata (T_a,T_b) that were randomly selected to interact in simulations of an open-ended multi-state automata population (see Section 12.1.2).

12.1.1 Generating the interaction network for a two-state automata population

There were 3,508,129 possible interactions in a population of 1,873 unique 2-state automata. It was impractical to perform an interaction - the functional composition of the T_a,T_b automata, the minimisation of the product automata T_c, and the validation of T_c as an ϵ-machine - during a simulation. Instead the complete interaction network G for an exclusive two-state population was generated *a priori* to running any simulation. The construction of G would need to examine all 3.5 million possible interactions and to record in the interaction matrix which interactions resulted in a minimised automata type that was validated as an ϵ-machine. Examining each of these interactions serially would be impractical and so an algorithm was developed to parallelise the task of generating the two-state interaction network.

A parallel algorithm was developed and run on a single compute node of the University of Bristol's supercomputer (Blue Crystal). Each compute node consisted of 16 processor cores. The task of generating the interaction network was therefore packaged into 16 discrete packages of work of 116 automata each (representing the T_b automata). For example, Task 1 would examine the interactions involving the automaton types 1...116 acting as the T_b automata in interactions with each of the 1,873 two-state automaton types acting as the T_a automata in the functional composition operation $T_b \circ T_a = T_c$. Task 2 examined the automaton types 117...233 as the T_b automata interacting with each of the 1,873 automaton types acting as T_a. Each task would generate a 1873×116 matrix. Each task was allocated to a dedicated core on a Blue Crystal compute node - see Table 12.2.

On completion of all 16 tasks the interaction matrix (1873×1873) was constructed from the concatenation of each 1873×116 matrix generated from each task. The completed in-

teraction matrix was then used as a lookup table during the simulation which considerably shortened the execution time.

12.1.2 Handling automata interactions in an open-ended, unconstrained multi-state population

In an open-ended computation niche model (i.e. no restriction on the size and complexity of the automata that can be generated) - see Chapter 9 - it was impractical to re-construct the entire interaction network of the population for each novel automata type produced on each time step, especially as some of the automaton types that were being generated had up to 64 states. Consequently, the following procedure was used in the open-ended computation niche simulations:

1. Automata T_a and T_b selected from the population to interact.
2. The latest version of the interaction G is examined to see if a known interaction for T_a, T_b exists.
3a. If $G_{T_a,T_b} <> \emptyset$ and $G_{T_a,T_b} > 0$ then an interaction exists. The value at G_{T_a,T_b} represents the valid automata type produced from this interaction.
3b. If $G_{T_a,T_b} = 0$ then no interaction exists between automata T_a and T_b.
3c. If $G_{T_a,T_b} = \emptyset$ then this interaction has not yet been examined. Perform functional composition of T_a,T_b and minimise the resulting automata T_c. Check whether the minimised automata T_c is a valid ϵ-machine.
4a. If T_c is a valid ϵ-machine then this is a new automata type. Add it to the population and record the interaction that produced it at $G_{T_a,T_b} = T_c$.
4b. If T_c is not a valid ϵ-machine then discard this item and record an unsuccessful interaction at $G_{T_a,T_b} = 0$.

This procedure constructs the interaction network G as the simulation proceeds. This procedure is not an exhaustive search of all possible interactions within the population as was the case with the procedure described in Section 12.1.1.

12.2 Software implementation in MATLAB

All simulations and analysis were written in MATLAB (version: R2016b). The implementation of the Finitary Process Soup [36],[123] in MATLAB was written entirely by the author. The enhancements and extensions of the FPS model to what were subsequently called the Information Niche model and the Computation Niche model were also written entirely by the author. A dataset on the two-state interaction network was provided by Professor James Crutchfield at the University of California in Davis, United States to aid

with the test and validation of my Hopcroft minimisation implementation routine. All information and network measures used in this project were also implemented by the author in MATLAB and the external software library, the Java Information Dynamics Toolkit (JIDT) [142], was used to verify the results that I obtained from my own implementation of Shannon's information entropy [48]. Finally, the two papers [36],[123] were used to compare the results I obtained and as reported in Chapters 4 (the outcome of simulating a one-state automata population under well-mixed and zero-diffusivity conditions), Chapter 5 (the outcome of simulating a two-state automata population under well-mixed conditions) and Chapter 7 (the spatial lattice patterns formed by niche 1B).

The simulation software and documentation of how the information niche and computation niche model were implemented in MATLAB can be accessed from the Github open-source repository at https://github.com/rjcarte/Pathways2Autopoiesis.

12.3 Explanation of the difference between the information niche and computation niche results for a one-state well-mixed population

Why was niche 1D reproduced by the computation niche and not niche 1A?. The niche that emerged in the one-state computation niche model with no environmental noise was structurally similar to information niche 1D (i.e. no automata go extinct). Given that the parameter settings for the computation niche model were for a well-mixed population why was niche 1A not produced? This was investigated by examining the effect of the activity of the membrane on population dynamics, and an evaluation of the procedure for selecting the automata that would be produced and replaced on each iteration of the simulation.

Activity of the membrane. The randomly determined threshold of each membrane automata may have been 'perturbing' population dynamics in a way that was analogous to an influx of external automata in the information niche model. To examine this the randomly determined threshold parameter (r) was set to a constant value $r = 0$. With $r = 0$ a membrane automata would be active as long as it was receiving information from at least one of its incoming links. As such, all membrane automata were constantly active. This meant that all population automata were available to interact on every iteration of the simulation. Simulations showed that the rate at which the decaying population automata were being produced was now reduced when compared to when r was randomly determined. However, the decaying population automata did not go extinct as per niche 1A.

So, whilst the the membrane automata activation threshold effected population dynamics it did not produce niche $1A$.

Asynchronous update mode of the population. The computation niche model operated a synchronous update whereby all population automata that could be produced within a given iteration were produced and replaced existing population automata. By comparison, the information niche model operated an asynchronous update whereby only one population automaton (randomly selected) was produced from the interaction between two randomly selected population automata. The computation niche model was adjusted to run in asynchronous mode and this only had the effect of slowing down the rate at which the population evolved to a steady-state that was similar to niche $1D$.

Determining which population automata were produced. Examination of the selection procedure (sampling) used within the computation niche model showed that with $r > 0$ the size of the population that was available for sampling varied over time due to the activity of the membrane. By comparison, the information niche model was sampling from a constant population size. Hence, the computation niche model was partially sampling [1] of the population given that certain automata were not available for interactions (due to an inactive status of their equivalent membrane automata). Over time this partial sampling of the population had the effect of equalising the frequency distribution of the population automata and this effected the selection of automata that would interact. Consequently, the rate at which the lower frequency population automata were selected for interacting was boosted whilst the rate at which higher frequency population automata were selected was reduced. On average this meant that the selection of an automaton to be produced in a given time step was taken from a more uniform distribution. This selection process had the effect of producing lower frequency population automata more frequently than would have been the case in the information niche model - see the simulation results in Table 12.3 that compares the difference in the frequency with which each population automata was produced over 4×10^5 iterations. In the computation niche model the automaton types that went extinct in the information niche model (due to being produced less) were now being produced often enough to remain in the population.

Whilst this comparison of the two simulations was useful it did not explain why the computation niche model did not generate niche $1A$. A more detailed examination of the procedure for the selection of automata to interact in the computation niche model, showed that the synchronous mode of updating the population meant that the population didn't need to be sampled as all active population automata at a given time-step would

[1] Partial sampling is an acceptable feature of the computation niche model as it relates directly to the on/off switching activity of the membrane automata.

Automata Type	Information Niche	Computation Niche	Difference
T_1	29020	29054	34
T_2	27383	29087	1704
T_3	49035	40344	-8691
T_4	28787	29191	404
T_5	51138	40608	-10530
T_6	325	3854	3529
T_7	1165	11533	10368
T_8	27146	28902	1756
T_9	327	3843	3516
T_{10}	47276	40596	-6680
T_{11}	1144	11523	10379
T_{12}	48166	40283	-7883
T_{13}	1134	11754	10620
T_{14}	1136	11611	10475
T_{15}	86818	67817	-19001
Total	400,000	400,000	0

Table 12.3: Comparison of the number of times each automata was produced in a simulation over 4×10^5 iterations under well-mixed conditions. As can be seen in the 'Difference' column there was a significant increase in the production of the automata $T_2, T_6, T_7, T_9, T_{11}, T_{13}, T_{14}$ balanced against a significant decrease in the production of the automata $T_3, T_5, T_{10}, T_{12}, T_{15}$. These changes were due to the partial sampling that occurred in the computation niche as a result of the membrane exciting or inhibiting different automaton types in the population.

interact with other active population automata to produce new automata. However, when the computation niche model was in asynchronous mode the sampling was from a list of automata that could be produced at that time-step (dictated by the activated or deactivated status of membrane automata) rather than sampling the automata that were available to interact. This difference is important as these modes sample the population in different ways: sampling the list of automata that could be produced on a time-step (as per the computation niche) was actually selecting a single automata (T_c) from a partial interaction network G_ψ (ψ was the activation status of each membrane automata) whereas sampling the population to select the automata that would interact required two automata to be selected (T_a,T_b) from the frequency distribution f. Whilst this is not an issue with the synchronous update mode (as the assumption was that all interactions that could take place on a given time-step did occur) it did mean that sampling the interaction network with the computation niche in asynchronous mode (where only one interaction could occur) would not produce the same results as the information niche (which operated in asynchronous mode). To test this a simulation was run with the computation niche in asynchronous mode and with the selection of automata that were produced replaced with

the process for selecting two population automata to interact as per the information niche model. Furthermore, the activation threshold for membrane automata was set to $r = 0$ so they were always active and this ensured that the population was fully sampled on each time-step. The simulation result clearly showed the reproduction of niche $1A$.

In summary, with the computation niche model in asynchronous mode, with membrane automata permanently active and with the selection of automata to be produced on each time step determined from the selection of two automata to interact (as per the information niche model) then niche $1A$ was produced with the computation niche model.

The motivation for the above investigation was to confirm that the computation niche model was capable of re-producing the niches $1A$ and $1D$ as per the information niche model. This has been shown.

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